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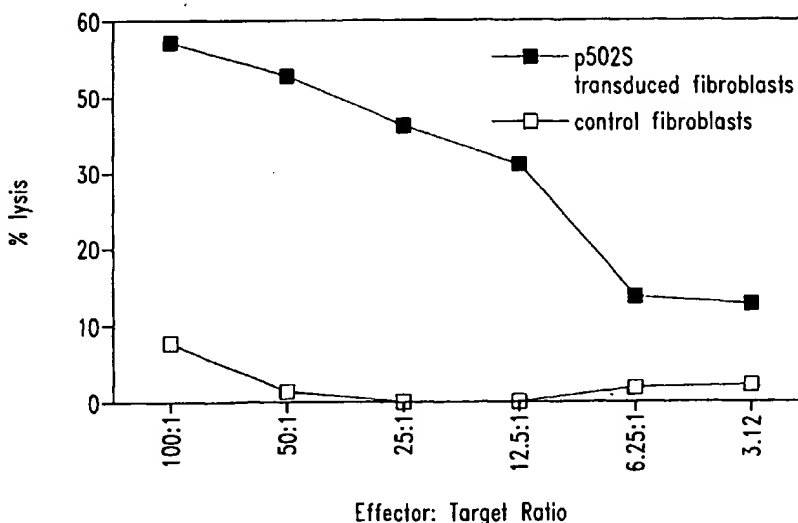
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[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate-specific proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate-specific protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate-specific protein, or mRNA encoding such a protein, in a sample are also provided.



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## COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

### 5 TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for  
10 prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress  
15 inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but  
20 these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate  
25 with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

### 30 SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the

diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate-specific protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-550.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate-specific protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines for prophylactic or therapeutic use are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate-specific protein; and (b) a physiologically acceptable carrier. In certain embodiments, the present invention provides monoclonal antibodies that specifically bind to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 522 and 541-550, together with monoclonal antibodies comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.



Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

5           Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

10           Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

15           Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that  
20 specifically react with a prostate-specific protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described  
25 above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with one or more of:  
(i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii)  
an antigen presenting cell that expresses such a polypeptide; under conditions and for a time  
30 sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate-specific protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

10 Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

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The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

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The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain

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embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that  
5 hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b)  
10 detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as  
15 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed  
20 herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The  
25 percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of  $\gamma$ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure  
30 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

5 Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse  
10 Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8<sup>+</sup> cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a <sup>51</sup>Cr release  
15 assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

20 Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

Figure 11 shows the results of an ELISA assay of antibody specificity to P501S  
25 peptides.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

30 SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

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SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12  
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SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14  
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SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16  
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SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860  
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

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SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)

5

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as

10 P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)

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SEQ ID NO: 165 is the determined cDNA sequence for P195

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SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-4896  
SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761  
30 SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762  
SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766  
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770

- SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
- SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772
- SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309
- SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
- 5 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
- SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
- SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
- SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
- SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
- 10 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
- SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
- SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
- SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
- SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
- 15 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
- SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
- SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
- SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
- SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
- 20 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
- SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
- SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
- SEQ ID NO: 220 is the determined cDNA sequence for 8-h11 rev
- SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
- 25 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
- SEQ ID NO: 223 is the determined cDNA sequence for P509S
- SEQ ID NO: 224 is the determined cDNA sequence for P510S
- SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
- SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
- 30 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
- SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
- SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13

- SEQ ID NO: 230 is the determined cDNA sequence for JTPN14  
SEQ ID NO: 231 is the determined cDNA sequence for JTPN23  
SEQ ID NO: 232 is the determined cDNA sequence for JTPN24  
SEQ ID NO: 233 is the determined cDNA sequence for JTPN25  
5 SEQ ID NO: 234 is the determined cDNA sequence for JTPN30  
SEQ ID NO: 235 is the determined cDNA sequence for JTPN34  
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35  
SEQ ID NO: 237 is the determined cDNA sequence for JTPN36  
SEQ ID NO: 238 is the determined cDNA sequence for JTPN38  
10 SEQ ID NO: 239 is the determined cDNA sequence for JTPN39  
SEQ ID NO: 240 is the determined cDNA sequence for JTPN40  
SEQ ID NO: 241 is the determined cDNA sequence for JTPN41  
SEQ ID NO: 242 is the determined cDNA sequence for JTPN42  
SEQ ID NO: 243 is the determined cDNA sequence for JTPN45  
15 SEQ ID NO: 244 is the determined cDNA sequence for JTPN46  
SEQ ID NO: 245 is the determined cDNA sequence for JTPN51  
SEQ ID NO: 246 is the determined cDNA sequence for JTPN56  
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64  
SEQ ID NO: 248 is the determined cDNA sequence for JTPN65  
20 SEQ ID NO: 249 is the determined cDNA sequence for JTPN67  
SEQ ID NO: 250 is the determined cDNA sequence for JTPN76  
SEQ ID NO: 251 is the determined cDNA sequence for JTPN84  
SEQ ID NO: 252 is the determined cDNA sequence for JTPN85  
SEQ ID NO: 253 is the determined cDNA sequence for JTPN86  
25 SEQ ID NO: 254 is the determined cDNA sequence for JTPN87  
SEQ ID NO: 255 is the determined cDNA sequence for JTPN88  
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1  
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2  
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2  
30 SEQ ID NO: 259 is the determined cDNA sequence for JP1B1  
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2  
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3

- SEQ ID NO: 262 is the determined cDNA sequence for JP1A4  
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5  
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6  
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6  
5 SEQ ID NO: 266 is the determined cDNA sequence for JP1B5  
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6  
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8  
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7  
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9  
10 SEQ ID NO: 271 is the determined cDNA sequence for JP1C10  
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9  
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12  
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12  
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11  
15 SEQ ID NO: 276 is the determined cDNA sequence for JP1C11  
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12  
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12  
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12  
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2  
20 SEQ ID NO: 281 is the determined cDNA sequence for JP8H1  
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2  
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3  
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4  
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3  
25 SEQ ID NO: 286 is the determined cDNA sequence for JP8G4  
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6  
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6  
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5  
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8  
30 SEQ ID NO: 291 is the determined cDNA sequence for JP8C7  
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7  
SEQ ID NO: 293 is the determined cDNA sequence for P8D8

- SEQ ID NO: 294 is the determined cDNA sequence for JP8E7  
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8  
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8  
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10  
5 SEQ ID NO: 298 is the determined cDNA sequence for JP8C10  
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9  
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10  
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9  
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9  
10 SEQ ID NO: 303 is the determined cDNA sequence for JP8C12  
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11  
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12  
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12  
SEQ ID NO: 307 is the determined cDNA sequence for P711P  
15 SEQ ID NO: 308 is the determined cDNA sequence for P712P  
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23  
SEQ ID NO: 310 is the determined cDNA sequence for P774P  
SEQ ID NO: 311 is the determined cDNA sequence for P775P  
SEQ ID NO: 312 is the determined cDNA sequence for P715P  
20 SEQ ID NO: 313 is the determined cDNA sequence for P710P  
SEQ ID NO: 314 is the determined cDNA sequence for P767P  
SEQ ID NO: 315 is the determined cDNA sequence for P768P  
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes  
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5  
25 SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5  
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26  
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26  
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23  
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23  
30 SEQ ID NO: 332 is the determined full length cDNA sequence for P509S  
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)  
SEQ ID NO: 334 is the determined cDNA sequence for P714P

- SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)
- SEQ ID NO: 336 is the predicted amino acid sequence for P705P
- SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10
- SEQ ID NO: 338 is the amino acid sequence of the peptide p5
- 5 SEQ ID NO: 339 is the predicted amino acid sequence of P509S
- SEQ ID NO: 340 is the determined cDNA sequence for P778P
- SEQ ID NO: 341 is the determined cDNA sequence for P786P
- SEQ ID NO: 342 is the determined cDNA sequence for P789P
- SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo
- 10 sapiens MM46 mRNA
- SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA
- SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin
- 15 SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)
- SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)
- SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo
- 20 sapiens phosphoglucomutase-related protein (PGMRP)
- SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteasome subunit p40
- SEQ ID NO: 350 is the determined cDNA sequence for P777P
- SEQ ID NO: 351 is the determined cDNA sequence for P779P
- 25 SEQ ID NO: 352 is the determined cDNA sequence for P790P
- SEQ ID NO: 353 is the determined cDNA sequence for P784P
- SEQ ID NO: 354 is the determined cDNA sequence for P776P
- SEQ ID NO: 355 is the determined cDNA sequence for P780P
- SEQ ID NO: 356 is the determined cDNA sequence for P544S
- 30 SEQ ID NO: 357 is the determined cDNA sequence for P745S
- SEQ ID NO: 358 is the determined cDNA sequence for P782P
- SEQ ID NO: 359 is the determined cDNA sequence for P783P

- SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984
- SEQ ID NO: 361 is the determined cDNA sequence for P787P
- SEQ ID NO: 362 is the determined cDNA sequence for P788P
- SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994
- 5 SEQ ID NO: 364 is the determined cDNA sequence for P781P
- SEQ ID NO: 365 is the determined cDNA sequence for P785P
- SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.
- SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.
- 10 SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.
- SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.
- SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.
- 15 SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.
- SEQ ID NO: 381 is the determined cDNA sequence for B716P.
- SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
- 20 SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
- SEQ ID NO: 384 is the cDNA sequence for P1000C.
- SEQ ID NO: 385 is the cDNA sequence for CGI-82.
- SEQ ID NO: 386 is the cDNA sequence for 23320.
- SEQ ID NO: 387 is the cDNA sequence for CGI-69.
- 25 SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.
- SEQ ID NO: 389 is the cDNA sequence for 23379.
- SEQ ID NO: 390 is the cDNA sequence for 23381.
- SEQ ID NO: 391 is the cDNA sequence for KIAA0122.
- SEQ ID NO: 392 is the cDNA sequence for 23399.
- 30 SEQ ID NO: 393 is the cDNA sequence for a previously identified gene.
- SEQ ID NO: 394 is the cDNA sequence for HCLBP.
- SEQ ID NO: 395 is the cDNA sequence for transglutaminase.



SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

5 SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

10 SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

15 SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

20 SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.

25 SEQ ID NO:420 is the cDNA sequence for 22581.

SEQ ID NO:421 is the cDNA sequence for 22582.

SEQ ID NO:422 is the cDNA sequence for 22583.

SEQ ID NO:423 is the cDNA sequence for 22584.

SEQ ID NO:424 is the cDNA sequence for 22585.

30 SEQ ID NO:425 is the cDNA sequence for 22586.

SEQ ID NO:426 is the cDNA sequence for 22587.

SEQ ID NO:427 is the cDNA sequence for 22588.

- SEQ ID NO:428 is the cDNA sequence for 22589.  
SEQ ID NO:429 is the cDNA sequence for 22590.  
SEQ ID NO:430 is the cDNA sequence for 22591.  
SEQ ID NO:431 is the cDNA sequence for 22592.  
5 SEQ ID NO:432 is the cDNA sequence for 22593.  
SEQ ID NO:433 is the cDNA sequence for 22594.  
SEQ ID NO:434 is the cDNA sequence for 22595.  
SEQ ID NO:435 is the cDNA sequence for 22596.  
SEQ ID NO:436 is the cDNA sequence for 22847.  
10 SEQ ID NO:437 is the cDNA sequence for 22848.  
SEQ ID NO:438 is the cDNA sequence for 22849.  
SEQ ID NO:439 is the cDNA sequence for 22851.  
SEQ ID NO:440 is the cDNA sequence for 22852.  
SEQ ID NO:441 is the cDNA sequence for 22853.  
15 SEQ ID NO:442 is the cDNA sequence for 22854.  
SEQ ID NO:443 is the cDNA sequence for 22855.  
SEQ ID NO:444 is the cDNA sequence for 22856.  
SEQ ID NO:445 is the cDNA sequence for 22857.  
SEQ ID NO:446 is the cDNA sequence for 23601.  
20 SEQ ID NO:447 is the cDNA sequence for 23602.  
SEQ ID NO:448 is the cDNA sequence for 23605.  
SEQ ID NO:449 is the cDNA sequence for 23606.  
SEQ ID NO:450 is the cDNA sequence for 23612.  
SEQ ID NO:451 is the cDNA sequence for 23614.  
25 SEQ ID NO:452 is the cDNA sequence for 23618.  
SEQ ID NO:453 is the cDNA sequence for 23622.  
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.  
SEQ ID NO:455 is the cDNA sequence for LIM protein.  
SEQ ID NO:456 is the cDNA sequence for a known gene.  
30 SEQ ID NO:457 is the cDNA sequence for a known gene.  
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:459 is the cDNA sequence for 23045.

SEQ ID NO:460 is the cDNA sequence for 23032.

SEQ ID NO:461 is the cDNA sequence for 23054.

SEQ ID NO:462-467 are cDNA sequences for known genes.

SEQ ID NO:468-471 are cDNA sequences for P710P.

5 SEQ ID NO:472 is a cDNA sequence for P1001C.

SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).

SEQ ID NO: 474 is the determined cDNA sequence for a second splice variant of P775P (referred to as 19947).

10 SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).

SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).

15 SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 479 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 475.

20 SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

25 SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

30 SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

- SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.
- SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.
- SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.
- SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.
- SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.
- SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.
- SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.
- SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.
- SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P. SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.
- SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.
- SEQ ID NO: 526 is the full-length cDNA sequence for P790P.
- SEQ ID NO: 527 is the predicted amino acid sequence for P790P.
- SEQ ID NO: 528 & 529 are PCR primers.
- SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.
- SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.
- SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.
- SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.
- SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.
- SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.
- SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.
- SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.
- SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.
- SEQ ID NO: 539 is the peptide P501S-370.
- SEQ ID NO: 540 is the peptide P501S-376.
- SEQ ID NO: 541-550 are epitopes of P501S.
- SEQ ID NO: 551 corresponds to amino acids 543-553 of P501S.

## DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate-specific polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate-specific protein or a variant thereof. A "prostate-specific protein" is a protein that is expressed in normal prostate and/or prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a non-prostate normal tissue, as determined using a representative assay provided herein. Certain prostate-specific proteins are proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate-specific proteins. Sequences of polynucleotides encoding certain prostate-specific proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Sequences of polypeptides comprising at least a portion of a prostate-specific protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

## PROSTATE-SPECIFIC PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate-specific protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred

polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate-specific protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate-specific protein. Polynucleotides complementary to any such sequences are also  
5 encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the  
10 present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate-specific protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions  
15 and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate-specific protein or a portion thereof. The  
20 term "variants" also encompasses homologous genes of xenogenic origin.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local  
25 regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the  
30 Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices

for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) *Unified Approach to Alignment and Phylogenesis* pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate-specific protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such

as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example,  
5 a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate-specific than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997).  
10 Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate-specific cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

15 An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate-specific cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes.  
20 Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with <sup>32</sup>P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A*  
25 *Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The  
30 complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into



a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments; using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate-specific protein are provided in SEQ ID NO:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536.

Isolation of these polynucleotides is described below. Each of these prostate-specific proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis.

5 Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate-specific protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain  
10 portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate-specific polypeptide, and administering the transfected cells to the patient).

15 A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a protein. Antisense technology can be used to control gene expression  
20 through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of  
25 the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30  
30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'

ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

5 Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector  
10 will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for  
15 therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). The polynucleotides may also be administered as naked plasmid vectors.  
20 Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary  
25 skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane  
30 vesicle). The preparation and use of such systems is well known in the art.

## PROSTATE-SPECIFIC POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate-specific protein or a variant thereof, as described herein. As noted above, a "prostate-specific protein" is a protein that is expressed by normal prostate and/or prostate tumor cells. Proteins that are prostate-specific proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate-specific protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate-specific protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the

immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example,  $^{125}\text{I}$ -labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate-specific protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate-specific protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino

acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, higher eukaryotic and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known prostate-specific protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner),

preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are

located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its



original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector  
5 that is not a part of the natural environment.

#### BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate-specific protein. As used herein, an  
10 antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate-specific protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate-specific protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding  
15 constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known in the art.

20 Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate-specific protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals  
25 without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the  
30 above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Most preferably, antibodies employed in the inventive methods have the ability to induce lysis of tumor cells by activation of complement and mediation of antibody-dependent cellular cytotoxicity (ADCC). Antibodies of different classes and subclasses differ in these properties. For example, mouse antibodies of the IgG2a and IgG3 classes are capable of activating serum complement upon binding to target cells which express the antigen against which the antibodies were raised, and can mediate ADCC.

Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells

and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are  
5 selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse.  
10 Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

The preparation of mouse and rabbit monoclonal antibodies that specifically bind to  
15 polypeptides of the present invention is described in detail below. However, the antibodies of the present invention are not limited to those derived from mice. Human antibodies may also be employed in the inventive methods and may prove to be preferable. Such antibodies can be obtained using human hybridomas as described by Cote *et al.* (Monoclonal Antibodies and Cancer Therapy, Alan R. Lisa, p. 77, 1985). The present invention also encompasses antibodies made by  
20 recombinant means such as chimeric antibodies, wherein the variable region and constant region are derived from different species, and CDR-grafted antibodies, wherein the complementarity determining region is derived from a different species, as described in US Patents 4,816,567 and 5,225,539. Chimeric antibodies may be prepared by splicing genes for a mouse antibody molecule having a desired antigen specificity together with genes for a human antibody molecule having the  
25 desired biological activity, such as activation of human complement and mediation of ADCC (Morrison *et al. Proc. Natl. Acad. Sci. USA* 81:6851, 1984; Neuberger *et al. Nature* 312:604, 1984; Takeda *et al. Nature* 314:452, 1985).

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard  
30 techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*,

Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to

Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

5           It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or  
10   linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent  
15   No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating  
20   compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of  
25   a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

#### T CELLS

30           Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate-specific protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral

blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEX™ system, available from Nexell Therapeutics Inc., Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated  
5 humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate-specific polypeptide, polynucleotide encoding a prostate-specific polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate-specific  
10 polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate-specific polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a  
15 variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell  
20 proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate-specific polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of  
25 the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate-specific polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Prostate-specific protein-specific T cells may be expanded using  
30 standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a prostate-specific polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate-specific polypeptide, or a short peptide  
5 corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate-specific polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate-specific protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

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#### PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds  
15 and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally  
20 described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the  
25 composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression  
30 systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression

in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA



or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10 ) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example,

an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent  
5 adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release  
10 formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix  
15 and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical  
20 compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the  
25 antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or  
30 progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy,

*Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take-up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface  
5 receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone  
10 marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into  
15 dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this  
20 nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II  
25 MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a prostate-specific protein (or portion or other variant thereof) such that the prostate-specific polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex*  
30 *vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection

that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells  
5 with the prostate-specific polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of  
10 the polypeptide.

#### CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical  
15 compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor.  
20 Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react  
25 against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not  
30 necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer

cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate  
5 antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in*  
10 *vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte,  
15 fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies  
20 have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back  
25 into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established  
30 using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered

over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50%  
5 above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-  
10 vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active  
15 compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate-specific protein generally correlate with an improved clinical outcome. Such immune responses may generally be  
20 evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or  
25 more prostate-specific proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the  
30 agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer.

In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g., Harlow and Lane, 5 Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized  
10 on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G,  
15 protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full  
20 length prostate-specific proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or  
25 disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization"  
30 refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a

membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of  
5 binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the  
10 binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may  
15 be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The  
20 amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween  
25 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer.  
30 Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by



assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains  
5 a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of  
10 time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group  
15 (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a  
20 signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is  
25 determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest  
30 to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along

the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate-specific polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate-specific protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate-specific protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a prostate-specific polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that

expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate-specific polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate-specific polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate-specific protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate-specific protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate-specific protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate-specific protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Techniques for both PCR based assays and hybridization assays

are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate-specific protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for proteins provided herein may be combined with assays for other known tumor antigens.

## DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For  
5 example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate-specific protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or  
10 indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate-specific protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate-specific protein. Such an oligonucleotide may be used, for example, within a PCR or  
15 hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate-specific protein.

The following Examples are offered by way of illustration and not by way of limitation.

## EXAMPLES

### EXAMPLE 1

#### 5 ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate  
10 tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning  
kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol.  
Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and  
total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the  
manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA  
15 purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-  
strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was  
synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with  
NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the  
cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into  
20 ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was  
prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by  
determining the number of independent colonies, the percentage of clones that carried insert, the  
average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$   
25 independent colonies, with 70% of clones having an insert and the average insert size being 1745  
base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69%  
of clones having inserts and the average insert size being 1120 base pairs. For both libraries,  
sequence analysis showed that the majority of clones had a full length cDNA sequence and were  
synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

30 cDNA library subtraction was performed using the above prostate tumor and normal  
pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some  
modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as

follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor  
5 expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid  
10 sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and  
15 mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

20 Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21,  
25 K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified  
30 human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA



library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show  
5 some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid  
10 sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided  
15 in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating  
20 sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in  
30 SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated

clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 5 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further 10 analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the 15 identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 20 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA<sup>+</sup> RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D- 25 4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

30 cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni,

Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively.

## EXAMPLE 2

### DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each

reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue  
5 (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found  
10 to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other  
15 tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of  
20 prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

25 RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors  
30 and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney,

but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following  
5 normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues  
10 tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in  
15 normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in  
20 prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and  
25 expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was  
30 found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

### EXAMPLE 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences  
5 for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the  
10 isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-  
15 170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA  
20 sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary  
25 (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a  
30 portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of

2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.



An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX\_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The putative full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 525.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483.

Subsequent studies led to the identification of a genomic region on chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led

to the identification of a potential open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

#### EXAMPLE 4

##### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

#### EXAMPLE 5

##### FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the

subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most

recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350, 351 and 353-365.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

## EXAMPLE 6

## PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

5           6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

          Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID  
10 NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A<sup>b</sup> binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (RPMI-1640; Gibco  
15 BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL),  $2 \times 10^{-5}$  M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells ( $5 \times$   
20  $10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

          P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb  
25 tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with P502S than against control fibroblasts. An example is presented in  
30 Figure 1.

          This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice  
5 were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2  
10 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 µg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on  
15 the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2Kb were immunized as described  
20 by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5µg of P1S #10 and 120µg of an I-A<sup>b</sup> binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (as described above) and cultured  
25 in the presence of irradiated (3000 rads) P1S#10-pulsed (2µg/ml P1S#10 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later cells ( $5 \times 10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were  
30 restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

#### EXAMPLE 7

##### 10 PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100  $\mu$ g P501S in the vector VR1012 either intramuscularly or intradermally. 15 The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at 20 least one naturally processed HLA-A2-restricted CTL epitope.

#### EXAMPLE 8

##### 25 ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8<sup>+</sup> T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van 30 Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8<sup>+</sup> T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a  $\gamma$ -interferon



ELISPOT assay (*see* Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on  $10^4$  fibroblasts in the presence of 3  $\mu\text{g/ml}$  human  $\beta_2$ -microglobulin and 1  $\mu\text{g/ml}$  P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml  $\gamma$ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a  $\gamma$ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

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## EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES  
IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8<sup>+</sup> cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts retrovirally transduced

to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (<sup>51</sup>Cr release) and interferon-gamma production (Interferon-gamma Elispot; see above and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

#### EXAMPLE 10

##### IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE-SPECIFIC ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 µg of p5 peptide together with 140 µg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived

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Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- $\gamma$  ELISPOT analysis as described above. Using a panel of  
5 HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a  
10 multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3  $\mu$ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8+ T cell lines were identified that  
15 specifically produced interferon- $\gamma$  when stimulated with P501S and CD80-transduced autologous fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- $\gamma$  in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

20 To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN- $\gamma$  ELISPOT assays against these A2Kb targets transduced with the "library" of P501S  
25 fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were  
30 also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN- $\gamma$  assay. Only peptides

P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.

5 In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40  
10 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as  
15 demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-  
20 P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

### EXAMPLE 13

#### IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

25

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in  
30 prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences

SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

5

Table I  
Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-Iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97%

of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

#### EXAMPLE 14

##### IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which



expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II

Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups:

- 10 Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group
- 15 libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III  
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV  
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57
439	22851	PAP

440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

## EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY  
ANALYSIS

5

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened  
10 using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-461 represent novel genes. The others (SEQ ID NO: 454-458 and 461-467) correspond to known sequences.

15

## EXAMPLE 16

## FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

20

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane

filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four  
5 sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene.

## EXAMPLE 17

### PROTEIN EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

This example describes the expression and purification of the prostate-specific antigen P501S in *E. coli*, baculovirus and mammalian cells.

#### a) Expression in *E. coli*

15

Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an  
20 antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min,  
25 and lastly by 1 cycle of 72°C for 10 min. The PCR product was cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

30

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The resulting culture was induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A

(Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

5           An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR  
10       product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as Ra12-P501S-N) was confirmed by DNA sequencing.

          The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands  
15       were also observed, probably due to aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

          A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of the *M. tuberculosis* antigen  
20       Ra12 (SEQ ID NO: 484) was prepared as follows. P501S DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

25       The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C fusion was used for expression in BL21CodonPlus induced by CE6 phage.

b) Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD\_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in mammalian cells

Full-length P501S (553AA) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The Fugene/DNA mixture

was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 µl of GenePorter was diluted in 500 µl of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 µg of plasmid DNA that was diluted in 500 µl of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

#### EXAMPLE 18

##### PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

###### **a) Preparation and Characterization of Antibodies against P501S**

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to



generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant ( $\mu\text{g/ml}$ )
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis.

Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1  $\mu\text{g/ml}$ , followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate

specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr.

HRP-labeled anti-mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L) Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors, 5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

#### **b) Preparation and Characterization of Antibodies against P503S**

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits

and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

5

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows.

The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further

15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception  
5 of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

10 Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat  
15 anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal,  
20 breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary,  
25 pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal  
30 antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the

appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

5 **c) Preparation and Characterization of Antibodies against P703P**

Rabbits were immunized with either a truncated (P703Ptrl; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptrl attached to a solid support. Rabbit monoclonal  
10 antibodies were isolated using SLAM technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

15

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal  
20 antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

25 The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk<sup>-/-</sup> cells either untransfected or transfected with a plasmid

expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

#### EXAMPLE 19

##### CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as

described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparagine, was synthesized as described above. A Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (i.e. intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM



sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C. Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by  
5 SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma  
10 membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter  
15 plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with  
20 phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates  
25 were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

30 In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above.

To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server (<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al. Science* 274:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

## CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID No: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

4. An isolated polynucleotide encoding at least 15 contiguous amino acid residues of a prostate-specific protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the protein  
5 comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413,  
10 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate-specific protein, or a  
15 variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396,  
20 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one  
25 of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530,  
30 531, 533, 535 and 536.

7. An isolated polynucleotide comprising a sequence that hybridizes under moderately stringent conditions to a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate-specific protein, the protein comprising an amino acid sequence encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536 or a complement of any of the foregoing polynucleotide sequences.

12. A monoclonal antibody that specifically binds to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 519, 520, 522 and 539-551.

5 13. A monoclonal antibody comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.

14. A fusion protein comprising at least one polypeptide according to  
10 claim 1.

15 15. A fusion protein according to claim 14, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

16 16. A fusion protein according to claim 14, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

17. A fusion protein according to claim 14, wherein the fusion protein  
20 comprises an affinity tag.

18. An isolated polynucleotide encoding a fusion protein according to claim 14.

25 19.. A pharmaceutical composition comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to any one of claims 11-13;
- 30 (d) a fusion protein according to claim 14; and

(e) a polynucleotide according to claim 18.

20. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- 5 (a) a polypeptide according to claim 1;  
(b) a polynucleotide according to claim 4;  
(c) an antibody according to any one of claims 11-13;  
(d) a fusion protein according to claim 14; and  
(e) a polynucleotide according to claim 18.

10

21. A vaccine according to claim 20, wherein the immunostimulant is an adjuvant.

22. A vaccine according to claim 20, wherein the immunostimulant  
15 induces a predominantly Type I response.

23. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 19.

20

24. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 20.

25. A pharmaceutical composition comprising an antigen-presenting cell  
25 that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

26. A pharmaceutical composition according to claim 25, wherein the antigen presenting cell is a dendritic cell or a macrophage.

27. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with an immunostimulant.

5 28. A vaccine according to claim 27, wherein the immunostimulant is an adjuvant.

29. A vaccine according to claim 27, wherein the immunostimulant induces a predominantly Type I response.

10

30. A vaccine according to claim 27, wherein the antigen-presenting cell is a dendritic cell.

31. A method for inhibiting the development of a cancer in a patient,  
15 comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide encoded by a polynucleotide recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, and thereby inhibiting the development of a cancer in the patient.

20

32. A method according to claim 31, wherein the antigen-presenting cell is a dendritic cell.

33. A method according to any one of claims 23, 24 and 31, wherein the  
25 cancer is prostate cancer.

34. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate-specific protein, wherein the protein comprises an amino acid sequence that is  
30 encoded by a polynucleotide sequence selected from the group consisting of:



(i) polynucleotides recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

5            wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate-specific protein from the sample.

35.        A method according to claim 34, wherein the biological sample is  
10    blood or a fraction thereof.

36.        A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

15

37.        A method for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with at least one component selected from the group consisting of:

(i)        a polypeptide according to claim 1;

20            (ii)        a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

(iii)       a polynucleotide encoding a polypeptide of (i) or (ii); and

(iv)       an antigen presenting cell that expresses a polypeptide of (i) or (ii),

25            under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

38.        An isolated T cell population, comprising T cells prepared according to the method of claim 37.

30

39. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 38.

5 40. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- 10 (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- 15 (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20

41. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

- 25 (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;
- 30 (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

(iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells; and

5 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

42. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

10 (a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-111,  
15 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

20 (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

43. A method according to claim 42, wherein the binding agent is an antibody.

25

44. A method according to claim 43, wherein the antibody is a monoclonal antibody.

45. A method according to claim 42, wherein the cancer is prostate  
30 cancer.

46. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- 5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;
- 10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the  
15 amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

47. A method according to claim 46, wherein the binding agent is an antibody.

20

48. A method according to claim 47, wherein the antibody is a monoclonal antibody.

49. A method according to claim 46, wherein the cancer is a prostate  
25 cancer.

50. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- 30 (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein,

wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

5 (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

10

51. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

15

52. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

20

53. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 25 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from 30 the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

5                    54. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

                    55. A method according to claim 53, wherein the amount of  
10 polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

                    56. A diagnostic kit, comprising:  
                    (a) one or more antibodies according to claim 11; and  
15                    (b) a detection reagent comprising a reporter group.

                    57. A kit according to claim 56, wherein the antibodies are immobilized on a solid support.

20                    58. A kit according to claim 56, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

                    59. A kit according to claim 56, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups,  
25 enzymes, biotin and dye particles.

                    60. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is  
30 encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45,

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61. A oligonucleotide according to claim 60, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536.

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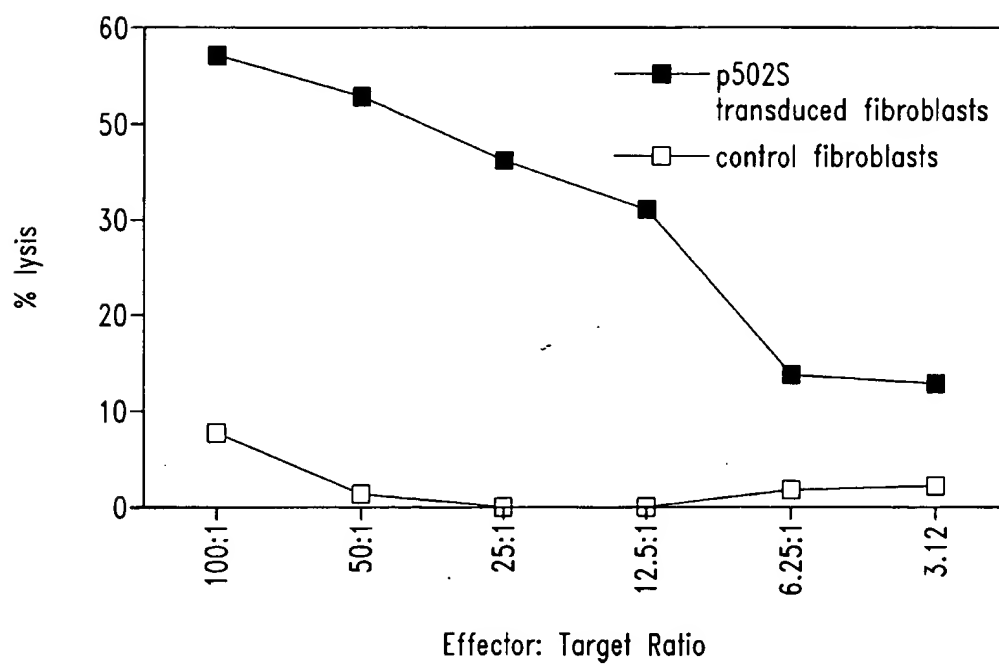
62. A diagnostic kit, comprising:  
(a) an oligonucleotide according to claim 61; and  
(b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

20

63. A host cell according to claim 10, wherein the cell is selected from the group consisting of: *E. coli*, baculovirus and mammalian cells.

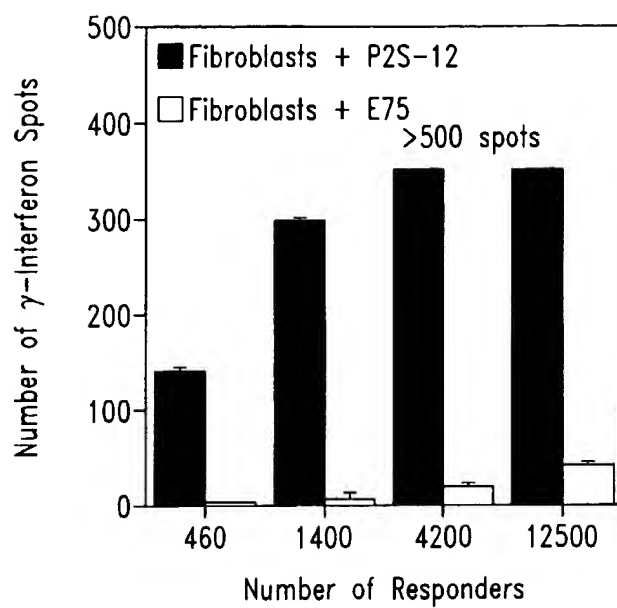
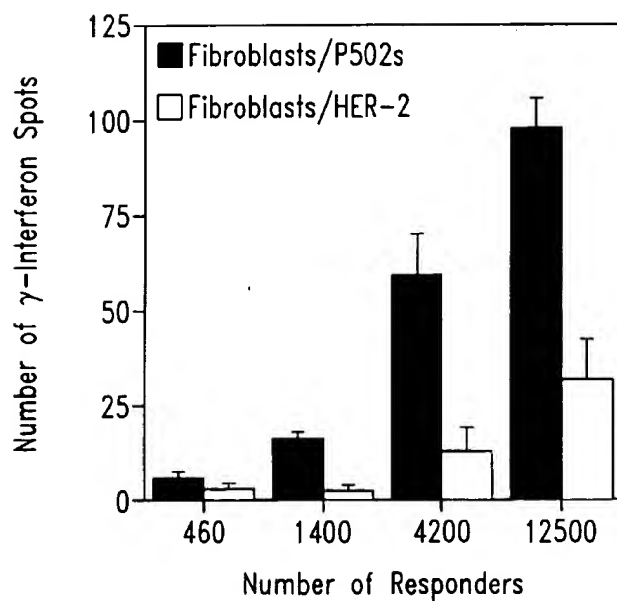
64. A recombinant protein produced by a host cell according to claim 10.

25



*Fig. 1*



*Fig. 2A**Fig. 2B*

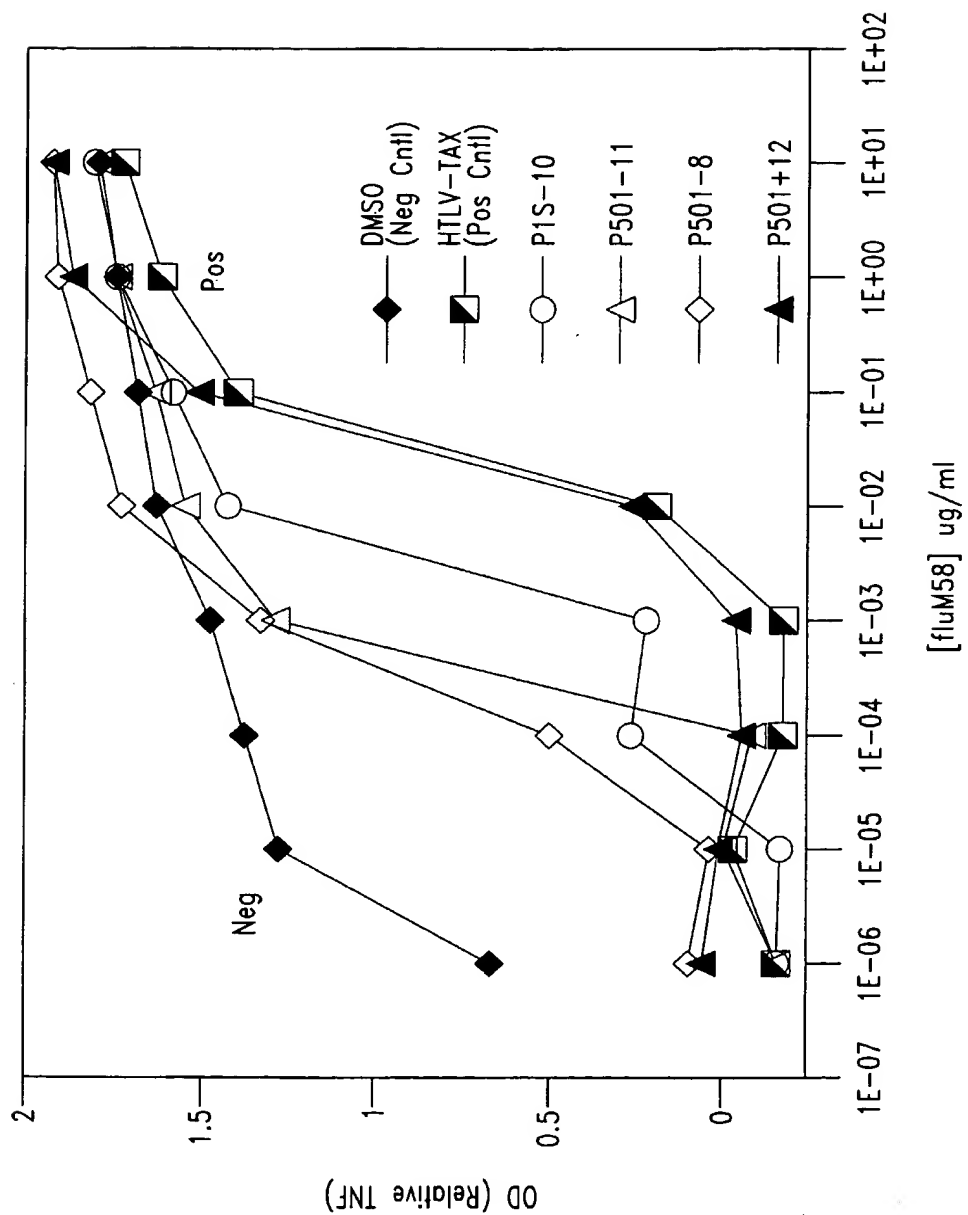
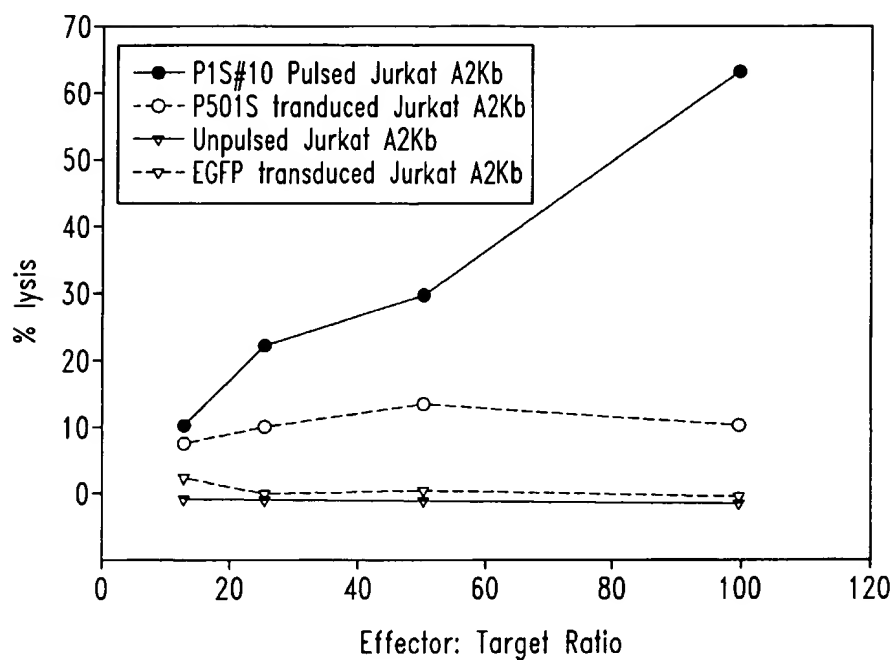
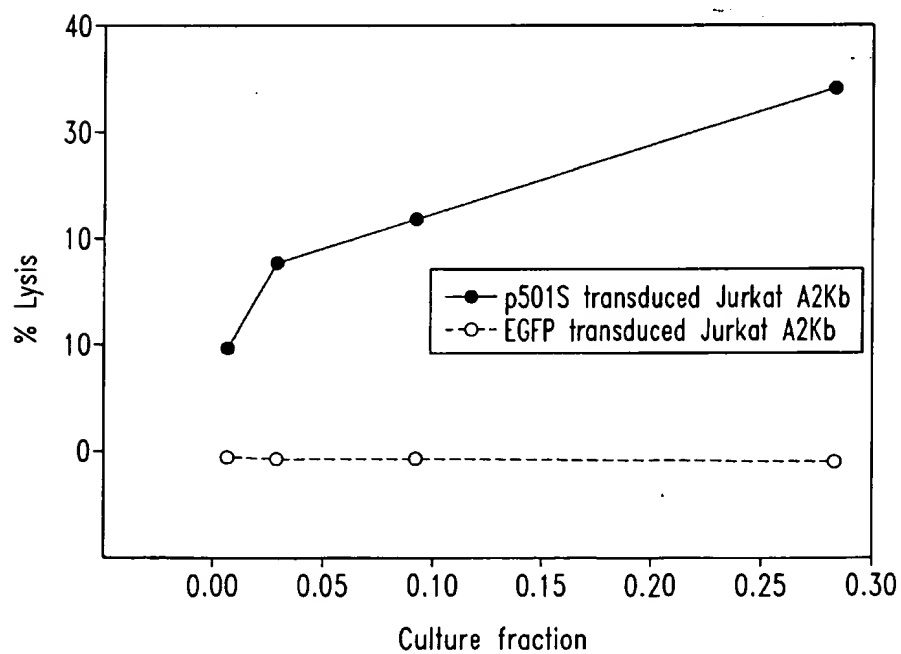
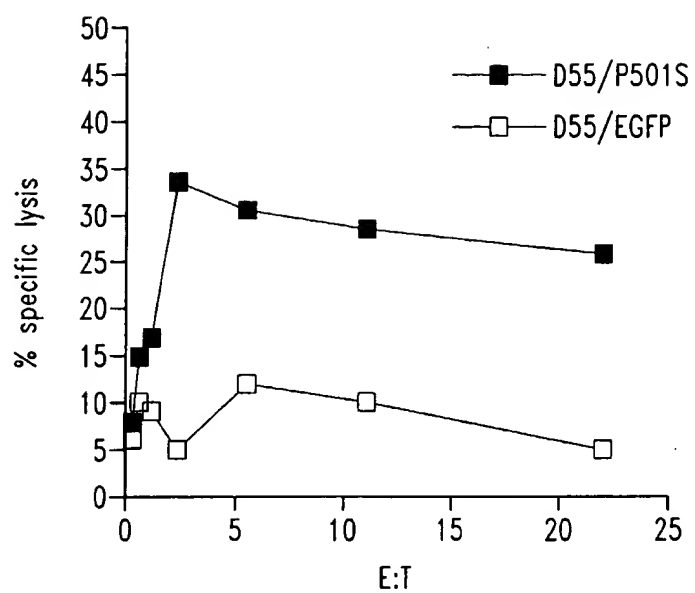
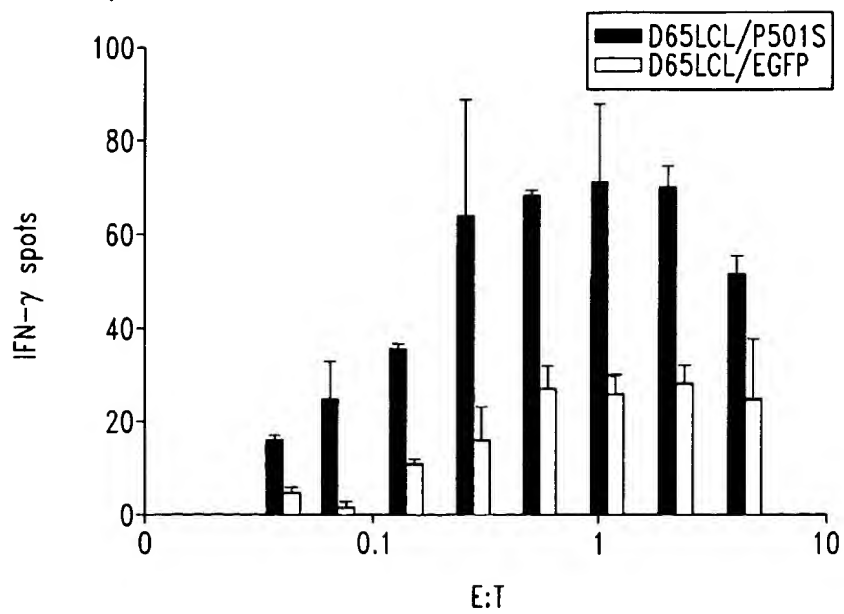
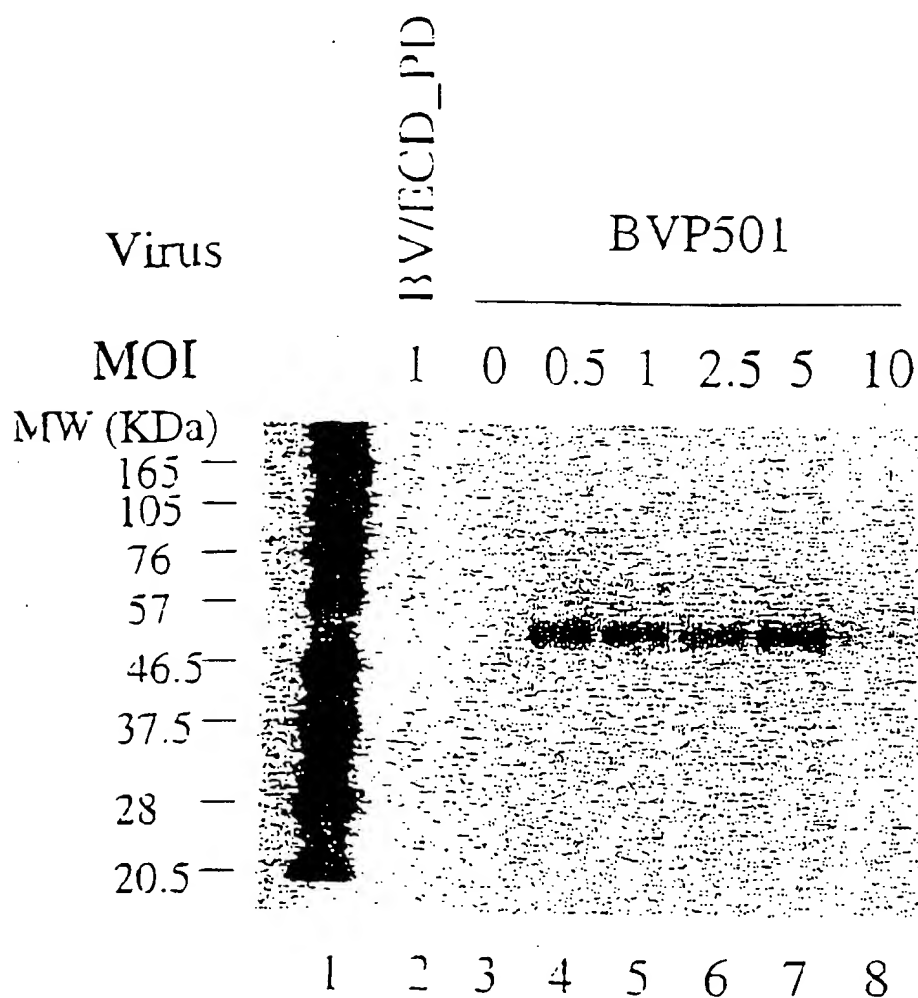


Fig. 3

*Fig. 4**Fig. 5*

*Fig. 6A**Fig. 6B*

# Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 8-well plate were infected with an unrelated control virus BV/ECD\_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7



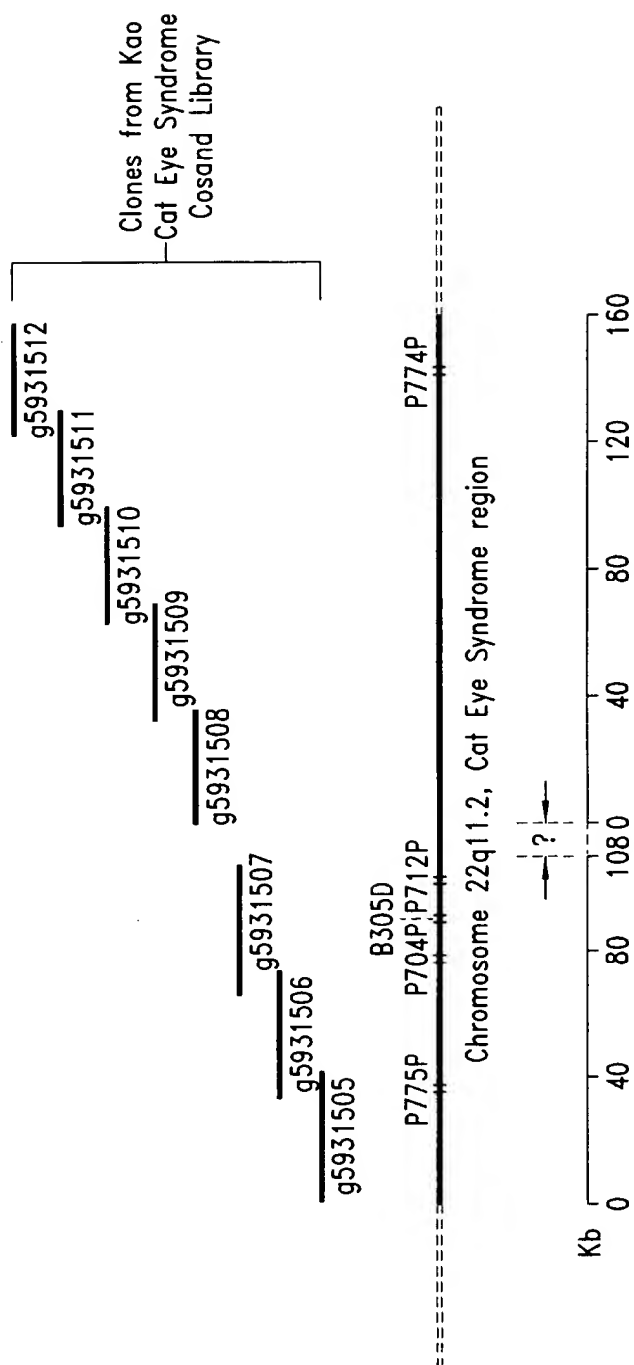
Schematic of P501S with predicted  
transmembrane, cytoplasmic, and extracellular regions

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Underlined sequence: Predicted transmembrane domain; **Bold sequence**:  
 Predicted extracellular domain; *Italic sequence*: Predicted intracellular  
 domain. Sequence in bold/underlined: used generate polyclonal rabbit  
 serum

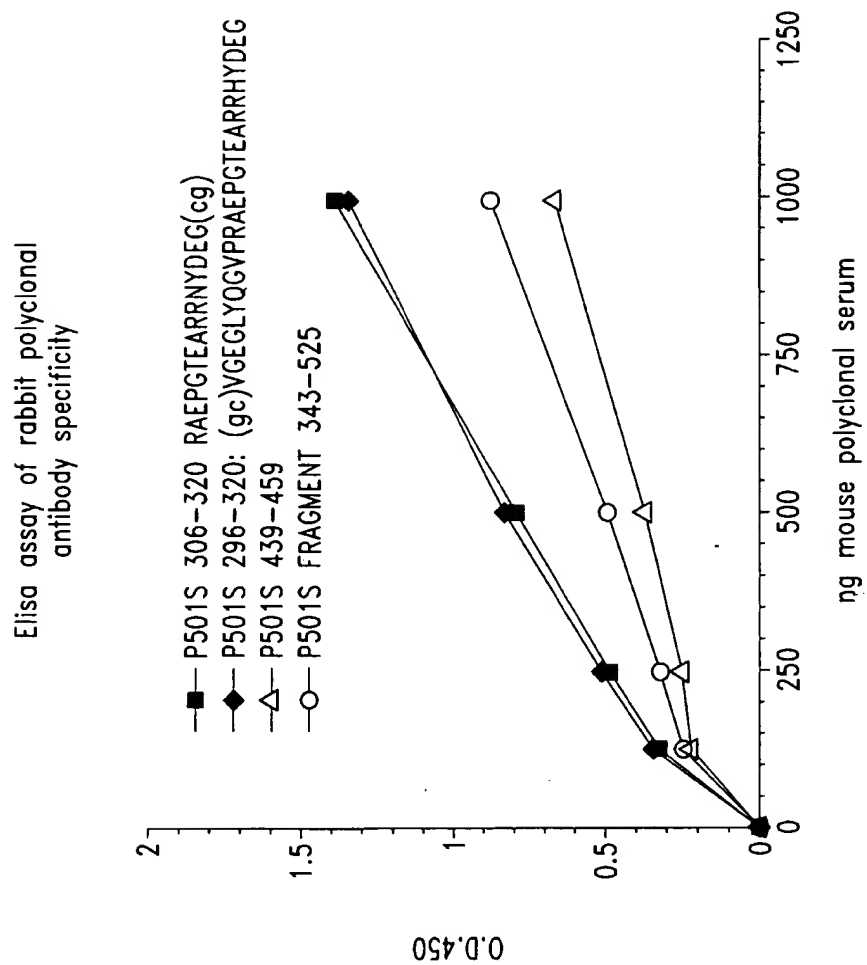
Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon  
 (1998) Principles Governing Amino Acid Composition of Integral Membrane  
 Proteins: Applications to topology Prediction. J.Mol Biol. 283, 489-506.

*Fig. 9*



*Fig. 10*



*Fig. 11*

## SEQUENCE LISTING

<110> Corixa Corporation  
 Xu, Jiangchun  
 Dillon, Davin C.  
 Mitcham, Jennifer L.  
 Harlocker, Susan Louise  
 Jiang Yuqui  
 Reed, Steven G.  
 Kalos, Michael  
 Fanger, Gary  
 Retter, Mark  
 Solk, John  
 Day, Craig  
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 Wang, Aijun

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 DIAGNOSIS OF PROSTATE CANCER

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ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggctgt	gtagcgggta	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcggga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggctcgc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctcctag	gttcaatacc	420
actggtggcc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tgttatgtaa	480
aggatnccct	ngggatggga	aggcnatnaa	ggcctangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaetnttnng	gaaaagggtc	tacaggacta	gaaaccaaata	angaaaanta	atnntaangg	660
cnttatcntn	aaaggtnata	accnctccta	tnatcccacc	caatngnatt	ccccacncnn	720
acnattggat	nccccanttc	canaaaanggc	cnccecccg	tgnannccnc	cttttggttc	780
cttnantgan	ggttattcnc	ccctngentt	atcance			817

&lt;210&gt; 8

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 8

catttccggg	tttactttct	aaggaaagcc	gagcgggaagc	tgctaacgtg	ggaatcgggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgctcctggg	240
tggttgccg	angcctganc	cgctctgcct	tgctgcccc	angtgggccg	ccacccccgt	300
acctgcctgg	gtccaaacac	tgagccctgc	tggeggactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcggcc	ccccacctg	gttggccttg	420
tctttgangt	gagccccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacia	ccacannatg	cccggtcctc	cccggaacc	antccancc	tgngaaggat	540
caagnccctgn	atccactnnt	nctanaaccg	gcncncnccg	cngtggaaacc	cnccttntgt	600
tccttttct	tnagggttaa	tnnccgcttg	gccttnccan	ngtccctncn	nttttccnnt	660

gttnaaattg ttangcnccc nccnntcccn cnnenncnan cccgaccenn annttnnann	720
ncctgggggt nccnncngat tgaccenncc nccctntant tgcnttnggg nncnntgccc	780
ctttccctct nggganncg	799

<210> 9  
 <211> 801  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(801)  
 <223> n = A,T,C or G

<400> 9	
acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtgggttg	60
taangatgac actcccaaag gtggctcctga cagtggccca gatggacatg gggctcacct	120
caaggacaag gccaccaggt gcgggggccc aagcccacat gatccttact ctatgagcaa	180
aatccctgt gggggcttct ccttgaagtc cgccancagg gctcagtcct tggaccang	240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcnc gggcctcngn	300
caccatccc angacgcggc tacactnctg gacctccnc tccaccactt tcatgcgctg	360
ttcntacccg cgnatntgtc ccantgttt cngtgcenac tccancttct nggacgtgcg	420
ctacatacgc cgggancnc nctcccgtt tgteccatc cagtnccan caacaaattt	480
cncctantg caccnattec cacttttnc agntttcnc nncgngcttc cttntaaaag	540
ggttgancec cggaaaatnc cccaaagggg gggggccngg tacccaactn cccctnata	600
gctgaantcc ccatnaccnn gnetcnatgg anccntcctt tttaannacn ttctnaactt	660
gggaanance ctcgncctn ccccnctaa tccnccctg cnangnnct ccccnntcc	720
nccnnntng gcntntnann cnaaaaaggc ccnnancaa tctcctnnn cctcanttcg	780
ccanccctcg aaatcgccn c	801

<210> 10  
 <211> 789  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(789)  
 <223> n = A,T,C or G

<400> 10	
cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgctgtccc	60
acagtgtggc cgtggtgaca gcttcagccg cctcaccgg gttcaccttc tcagccctgc	120
agatccctgcc ctacacactg gcctccctct accaccggga gaagcaggtg ttccctgccca	180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttccctgc	240
caggccctaa gcctggagct cccttcccta atggacacgt ggggtgctgga ggcagtggcc	300
tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg	360
tggtgggtga gccaccgan gccagggtgg ttccgggccc gggcatctgc ctggacctcg	420
ccatccctgga tagtgettcc tgctgtccca ngtggcccca tccctgttta tgggtccat	480
tgccagctc agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt	540
ccatttact ttgtacaca ggtantattt gacaagaacg anttggccaa atactcagcg	600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactcccgc	660
tcctgttaac ccatggggc tgccggcttg gccgcaatt tctgttctg ccaaantnat	720
gtggtctctc gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng	780
gngttccc	789

<210> 11  
 <211> 772

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(772)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 11

```

cccaccctac ccaaataatta gacaccaaca cagaaaagct agcaatggat tcccttctac      60
tttgttaaat aaataagtta aatattttaa tgccctgtgtc tctgtgatgg caacagaagg      120
accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc      180
tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata      240
actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag      300
ctacattaaa cgaagctgca gggttaagggg cttanagatg ggaaaccagg tgactgagtt      360
tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc      420
ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc      480
ctccctgtat aagtccagac tgaaaccccc ttggaaggnc tccagtcagg cagccctana      540
aactggggaa aaaagaaaag gacgccccan cccccagctg tgcanctacg cacctcaaca      600
gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaaact nggggggggca      660
accccgccac ccnangggg gttaacagga ancnggnaa cntggaacct aatnaggca      720
ggccnccac ccnaatntt gctgggaaat ttttctccc ctaaattntt tc              772

```

&lt;210&gt; 12

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(751)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 12

```

gccccaatc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaa      60
agctgattga agcaaccctc tactttttgg tcgtgagcct tttgcttggg gcaggtttca      120
ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg      180
aagtanggtg agtcctcaaa atccgtatag ttgggtgaag cacagcactt gagccctttc      240
atggtggtgt tccacacttg agtgaagtct tctggggaac cataatcttt cttgatggca      300
ggcactacca gcaacgtcag ggaagtgtct agccattgtg gtgtacacca aggcgaccac      360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tncgaggggc      420
acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna      480
cnccggctgc gatgaagaaa tnacccnngc ttgacaaact tgcattggcag tggganccac      540
agtggcccna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg      600
ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct      660
tnatnaacnt gaacctgcn tngtggctcc tgttcaggnc cnnggcctga cttctnaann      720
aangaactcn gaagncccca cngganannc g              751

```

&lt;210&gt; 13

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(729)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 13

gagccaggcg	tccctctgcc	tgcccactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aagancctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcgggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgcat	ccggcggtgt	ggtcttagct	ctaggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcatcc	tcctcctcat	cttcattgct	420
gagggttcaa	tgctgtggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgctggtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaanact	tcactcaagt	540
gttggaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaaanagt	cctttccccc	atttctgttg	caattgacaa	660
acgtccccaa	cacagccaat	tgaaaacctg	cacccaaccc	aaanggttcc	ccaaccanaa	720
attnaagg						729

&lt;210&gt; 14

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (816)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 14

tgctcttcct	caaagttggt	cttggtgcca	taacaaccac	cataggtaaa	gcgggagcag	60
tgctcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgacagag	tcctgtgtct	120
ggcaggtcca	cgcagtcccc	ttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaag	180
ccactcgtgt	atttttcaca	ggcagcctcg	tccgacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaactg	ggtgggctga	300
cangtgccag	agcaactggg	atggcgctt	tccatggnan	gggccctgng	ggaaagtccc	360
tgancctcan	anctgcctct	caaangcccc	accttgacac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaaggtag	ttnttcttgt	tgcccaancc	anccccntaa	acaaactctt	480
gcanatctgc	tccngggggg	tctantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttggt	tgatnccgaa	gcnaaatct	ncnttctgc	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	gttgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnanctn	ccccctggtt	tggggttttt	720
cncnctecta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccacccac	gggttcngnt	ggttng			816

&lt;210&gt; 15

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (783)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgcctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtact	gtgctgtcca	240
ccaagcagac	agaagactac	tgctcgcac	ccaacaangt	gggtcgtgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360



```

gcttgggcaa caagaacaac taccttcggg aagaagagtg cattctancc tgtcnggggtg      420
tgcaaggtgg gcctttgana ngcanctctg gggctcangc gactttcccc cagggcccct      480
ccatggaaaag ggcgccatcca ntgttctctg gcacctgtca gccaccccag ttccgctgca      540
ncaatggctg ctgcatcnac antttctctg aattgtgaca acacccccca ntgcccccaa      600
ccctcccaac aaagcttccc tgttnaaaaa tacnccantt ggcttttnac aaacncccg      660
cncctcctnt tccccnntn aacaaagggc nctngcnttt gaactgccc n aaccnnggaa      720
tctnccnngg aaaaantncc ccccttgggt cctnnaancc cctccncaa anctncccc      780
ccc                                                                                   783

```

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<210> 16
<211> 801
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (801)
<223> n = A,T,C or G

```

```

<400> 16
gccccaatc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaa      60
agctgattga agcaaccctc tacttttttg tcgtgagcct tttgcttggt gcaggtttca      120
ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg      180
aagtaggggt agtccctcaa atccgtatag ttgggtgaag cacagcactt gagccctttc      240
atgggtgtgt tccacacttg agtgaagtct tccctgggaac cataatcttt ctgatggca      300
ggcactacca gcaacgtcag gaagtgtcga gccatttgtg tgtacaccaa ggcgaccaca      360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca      420
cacttgctct ccgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg      480
cengctgcga atgaaagaaa ntaccacgt tgacaaactg catggccact ggacgcagat      540
tggccgaan atcttcagaa aagggatgcc ccatcgattg aacacccana tgcccactgc      600
cnacagggct gcncncncn gaaagaatga gccattgaag aaggatcnc ntgggtcttaa      660
tgaactgaaa ccntgcatgg tggcccctgt tcagggctct tggcagtga ttctganaaa      720
aaggaacngc ntnagcccc ccaaangana aaacaccccc ggggtgttgc ctgaattggc      780
ggccaaggan ccctgcccen g                                                                                   801

```

```

<210> 17
<211> 740
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (740)
<223> n = A,T,C or G

```

```

<400> 17
gtgagagcca ggcgtccctc tgccctgcca ctcaagtggc acaccggga gctgttttgt      60
cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg      120
agccaccatg cagtgttca gcttcattaa gaccatgatg atcctcttca atttgctcat      180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc      240
ctttctgaag atcttcgggc cactgtcgtc cagtggccat cagtttgta acgtgggcta      300
cttctcctc gcagccggcg ttgtgtctt tgccttgggt ttcctgggct gctatggtgc      360
taagacggag agcaagtgtg cctcgtgac gttcttcttc atcctcctcc tcatcttcat      420
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct      480
gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc      540
aantntggaa caccnccatg aaaagggtc caatttctgn tggcttcccc aactataccg      600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttncc ccnttctgt      660
tgcaatgaaa acntccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa      720

```

caaaaaaant nnaagggttn

740

<210> 18  
 <211> 802  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(802)  
 <223> n = A,T,C or G

<400> 18  
 ccgctggttg cgctgtcca gngnagccac gaagca<sup>2</sup>gtc agcatacaca gcctcaatca 60  
 caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg 120  
 ggatacactt tacttttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180  
 gagcctctgt tagtggagga agattccggg cttcagctaa gtagtcagcg tatgtcccat 240  
 aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa 300  
 cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360  
 ggatgagtgt ggccagcgct gcccccttgg ccgacttggc taggagcaga aattgtcctc 420  
 ggttctgccc tgtcaccttc acttccgcac tcactactgc actgagtgtg ggggacttgg 480  
 gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc 540  
 gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cnetacttgc 600  
 aancctcgtc nggcccattg aattcaccnc accggaactn gtangatcca ctntttctat 660  
 aaccggnccg caccgcnnnt ggaactccac tcttnttnc tttacttgag ggtaaggtc 720  
 acccttnncg ttactttggt ccaaaccntn cntgtgtcg anatngtnaa tcnggnccna 780  
 tnccancnc atangaagcc ng 802

<210> 19  
 <211> 731  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(731)  
 <223> n = A,T,C or G

<400> 19  
 cnaagcttcc aggtnacggg ccgchnaacc tgaccnagg tancanaang cagnncgcgg 60  
 gagcccaccg tcacngngng gngtctttat nggagggggc ggagccacat cnetggacnt 120  
 cntgacccca actcccncc nncantgca gtgatgagtg cagaactgaa ggtnacgtgg 180  
 caggaaccaa gancaaannc tgctccnntc caagtcggcn nagggggcgg ggctggccac 240  
 gcncatccnt cnagtgtctgn aaagcccnnc cctgtctact tgtttggaga acngcnngga 300  
 catgcccagn gttanataac nggcnagag tnannttgcc tctcccttcc ggctgcgcan 360  
 cngtntgtct tagnggacat aacctgacta cttaactgaa cccnngaate tncnccccct 420  
 ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta 480  
 aagtgtaccc catncccaat gtntgctnga ngetctgncc tgcnttangt tcggtcctgg 540  
 gaagacctat caattnaagc tatgtttctg actgcctctt gtcctctgna acaanccacc 600  
 cnnnntcca agggggggnc ggcccccaat ccccccaacc ntnaattnan ttanccccn 660  
 ccccnggcc cggcctttta cnancntcn nnacngggna aaaccnnngc tttncccaac 720  
 nnaatccncc t 731

<210> 20  
 <211> 754  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (754)  
 <223> n = A,T,C or G

<400> 20  
 .tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60  
 caaccccctc ntccaaatnn ccntttccgg gnggggggttc caaacccaan ttanntttgg 120  
 annttaaatt aaatnttntt tggnggnnna anccnaatgt nangaaagtt naaccanta 180  
 tnancttnaa tncctggaaa cngtngntt ccaaaaatnt ttaaccctta antccctcgg 240  
 aaatngttna nggaaaaccc aantttctnt aaggttggtt gaaggntnaa tnaaaanccc 300  
 nnccaattgt ttttngccac gcctgaatta attggnnttc gntgttttcc nttaaaanaa 360  
 ggnnancccc ggttantnaa tcccccnnc cccaattata ceganttttt ttngaattgg 420  
 gancccnccg gaattaacgg ggnnnttccc tnttgggggg cnggnncccc cccctcggg 480  
 ggttngggg aggnncnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc 540  
 ccaggntgag nntnggggtt ncccccccc canggccctt ctcgnanagt tggggtttgg 600  
 ggggcctggg attttnttcc cctntttccc tcccccccc ccnggganag aggttngngt 660  
 tttgntcnnc ggccccnccn aaganctttn ceganttnan ttaaatecnt gcctnggcga 720  
 agtcenttgn agggntaaan ggccccctnn cggg 754

<210> 21  
 <211> 755  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (755)  
 <223> n = A,T,C or G

<400> 21  
 atcancccat gacccnaac nngggaccnc tcancggnc nnncnaccnc cggccnatca 60  
 nngtnagnnc actncnnttn natcacnccc cncnactac gccncnanc cnacgcnceta 120  
 nncanatncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn 180  
 ccagctgtcc nanaangcct nnnatacnng nnnatccaat ntgnancctc cnaagtattn 240  
 nncnncanat gattttctn anccgattac cctncccc tancecctcc ccccaacna 300  
 cgaaggcnct ggncnnaagg nngcgnccnc ccgctagntc ccenncaagt cncnnceta 360  
 aactcancn nattaacncc ttentgagta tcaactcccc aatctcacc tactcaactc 420  
 aaaaaanacn gatacaaaat aatncaagcc tgnattatnac actntgactg ggtctctatt 480  
 ttagnggtcc ntnaanctc ctaatacttc cagtctncc tcnccaattt cnaanggct 540  
 ctttcngaca gcatnttttg gtccccntt gggttcttan ngaattgcc ttentngaac 600  
 gggctcntct tttccttcgg ttanctggg tcnncggc cagttattat tccccnttt 660  
 aaattcntnc cntttanttt tggcnttca aacccccggc cttgaaaacg gccccctgg 720  
 aaaaggttgt tttganaaaa tttttgttt gttcc 755

<210> 22  
 <211> 849  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (849)  
 <223> n = A,T,C or G

<400> 22  
 tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt 60  
 acgtnggan taangcgacc cgantttctag gannccct aaaaatcanac tgtgaagatn 120

```

atcctgnnna  eggaanggtc  accggnggat  nntgctaggg  tgnccnetcc  cannnenttn  180
cataactcng  nggccctgcc  caccaccttc  ggcggcccng  ngncggggcc  cgggtcattn  240
gnnttaaccn  cactnngcna  ncggtttccn  nccccnncng  acccnggcga  tccggggtn  300
tctgtcttcc  cctgnagncn  anaaantggg  ccncggncce  ctttaccct  nnacaagcca  360
cngcctteta  ncencngccc  cccctccant  nngggggact  gccnanngt  ccgttntcng  420
nnaccccnnn  gggtnccctg  gttgtcgant  cnaccgnang  ccanggattc  cnaaggaagg  480
tgcgttnttg  gcccctacc  ttcgtncgg  nncacccttc  ccgaenanga  nccgtcccg  540
cncnncgnng  cctencctcg  caacaccgc  nctentcngt  ncggnnnccc  ccccaccgc  600
nccctcncnc  ngncgnannc  ctcncncnc  gtctcannca  ccaccccgcc  ccgccaggcc  660
ntcanccacn  ggnngacnng  nagnncntc  gcncgcgcgn  gcgnncctc  cgcncngaa  720
ctnctcngg  ccantnncgc  tcaancnna  cnaaacgcgc  ctgcgcggcc  cgnagcgncc  780
nccctcncga  gtcctcccg  ctccnacc  angnnttcn  cgaggacacn  nnaccccgcc  840
nncangcgg  849

```

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

```

gcgcgaaacta  tacttcgctc  gnactcgtgc  gcctcgtcnc  tcttttcctc  cgcaaccatg  60
tctgacnanc  ccgatttggc  ngatatacn  aagntcganc  agtccaaact  gantaacaca  120
cacacnncn  aganaaatcc  nctgccttc  anagtanacn  attgaacnng  agaaccangc  180
nggcgaatcg  taatnaggcg  tgcgcgcga  atntgtcncc  gtttattntn  ccagctcnc  240
ctnccnacc  tacntctcn  nagtgcncn  accctngtn  cgnaccccc  naggtcggga  300
tcgggttttn  nntgaccgng  cnnccctcc  cccctccat  nacgancnc  ccgcaccacc  360
nanngcncgc  ncccggnct  ctgcgcnc  ctgtcctntn  cccctgtngc  ctggcncngn  420
accgcattga  cctcgcncn  ctncnngaa  ncgnanacgt  ccgggttgnn  annancgctg  480
tgggnnngcg  tctgcncgc  gtccctccn  ncnnctcca  ccatcttct  taenggtct  540
ccncgcctc  tcnnncaenc  cctgggacgc  tntcctntgc  ccccttnac  tccccctt  600
cgnctgncc  cgnccccc  ntcatttnca  nacgntcttc  acaannncct  ggntnntcc  660
cnancnncn  gtcancnag  ggaaggngg  ggnncnntg  nttgacgttg  ngngangtc  720
cgaanantcc  tcnccntcn  cctaccct  cggcggnct  ctngttncc  aacttancaa  780
ntctcccccg  ngngcncntc  tcagcctcnc  cnccccnct  ctctgcantg  tntctgctc  840
tnaccnntac  gantnttcn  cncctcttt  cc  872

```

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

```

gcatgcaagc  ttgagtattc  tatagngtca  cctaaatanc  ttggcntaat  catggtcnta  60
nctgncttcc  tgtgtcaa  gtatacna  tanatatgaa  tctnatntga  caaganngta  120
tctnccatta  gtaacaantg  tntgtccat  cctgtcngan  canattccca  tnnatnccn  180
cgcattnccn  gcncantatn  taatngggaa  ntcnnntnnn  ncacnncat  ctatctncc  240
gcnccttgac  tggagagat  ggatnanttc  tntnttgacc  nacatgttca  tcttggtatn  300
aanaccccc  cgcngnccac  cggttngnng  cnagcncntc  ccaagacctc  ctgtggaggt  360

```

aacctgcgtc	aganncatca	aacntgggaa	accgcgnnc	angtnnaagt	ngnnncanan	420
gateccgtcc	aggnttnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagnnagc	480
gtgtccnanc	cnetcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cnencangaa	atcccnanc	600
ccnccctac	ccncttttg	gacngtgacc	aantcccga	gtncagtc	ggcngnctc	660
ccccaccgt	nncntggg	gggtgaanct	cngnntcanc	cngncgaggn	ntcgnaagga	720
accggnccn	ggncgaanng	ancnntcnga	agnccnct	cgtataaacc	cccctcncca	780
nccnancngnt	agntcccccc	cngggtncgg	aangg			815

<210> 25  
 <211> 775  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(775)  
 <223> n = A,T,C or G

<400> 25						
ccgagatgtc	tcgtccgtg	gccttagctg	tgctgcgct	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcattccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttgact	180
tactgaagaa	tgganagaga	attgaaaaag	tggagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctcntg	tactacactg	aattcacccc	caactgaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnncatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcntttta	antgatatgc	ntatacaccc	taccctttat	gnccccaat	480
tgtaggggtt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgccgt	cnccngttn	ngaattgttc	cnnaaccacg	gttggtctcc	ccaggtcncc	600
tcttacggaa	gggcctgggc	cnctttncaa	ggttggggga	accnaaaatt	tcnctntgc	660
cncccncca	cnntcttng	nnncanttt	ggaacccttc	cnattccct	tggcctcna	720
nccttnncta	anaaaacttn	aaancgtngc	naaannttn	acttcccccc	ttacc	775

<210> 26  
 <211> 820  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(820)  
 <223> n = A,T,C or G

<400> 26						
anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgcctt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcggtgagg	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	cnagatnan	cactgcttc	aagtgcaccc	360
ttcctacctg	acnaccagng	accnnnaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnnagcact	cactgcctcc	cccatggccg	tnccntccc	tggtcctgnc	aagggaagct	480
ccctgttga	attncgggga	naccaaggga	nnccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttcg	gccnntccc	tcttcttta	cacgccccct	nntactctc	600
tcctctntt	ntcctgncnc	acttttnacc	ccnnnatttc	ccttnattga	tcggannctn	660
ganattccac	tnncgcctnc	cntcnatcng	naanacnaaa	nactntctna	ccnggggat	720
gggnncctcg	ntcatcctct	cttttctnct	accnccnntt	ctttgcctct	ccttngatca	780

tccaaccntc gntggccntn cccccccnnn tccttttcccc

820

<210> 27  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(818)  
 <223> n = A,T,C or G

<400> 27  
 tctgggtgat ggcctcttcc tctcagggga cctctgactg ctctgggcca aagaatctct 60  
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120  
 ctgcggatgc tgtgacggac ccaaggggca aataggggtc caggggtccag ggaggggagc 180  
 ctgtgagca cttccgcccc tcacctgcc cagccctgc catgagctct gggtgggtc 240  
 tccgcctcca gggttctgct cttccangca ngccancaag tggcgctggg ccacactggc 300  
 ttcttctgct cccntccctg gctctganc tctgtcttcc tgtcctgtgc angcnccttg 360  
 gatctcagtt tccctcctc anngaactct gtttctgann tcttcantta actntgantt 420  
 tatnaccnan tggngctgtnc tgtcnnactt taatgggccc gaccggctaa tccctccctc 480  
 nctcccttcc anttcnnna accngcttnc cntctctcc ccntancccg ccngggaanc 540  
 ctcccttgcc ctnaccangg gccnnnaccg cccntnctn ggggggcnng gttnctncnc 600  
 ctgntnnccc cctcncnt tncctctgccc cncnncgc nngcannctc ncngtcccn 660  
 tnnctcttcn ngntcgnaa ngntcncntn tnnnnngcn ngntnntn tccctctcnc 720  
 cnnntgnang tnnntnnnc ncngnncccc nnnnnnnnn nggnntnnn tctnncngc 780  
 cccnncccc ngnattaagg cctcnnctc ccggccnc 818

<210> 28  
 <211> 731  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(731)  
 <223> n = A,T,C or G

<400> 28  
 aggaagggcg gaggatatt gtangggatt gagggatagg agnataangg gggaggtgtg 60  
 tccaacatg anggtgnngt tctcttttga angaggttg ngtttttann ccnggtgggt 120  
 gattnaacc cttgtatgg agnnaaagg ttnnaggat ttttcggctc ttatcagtat 180  
 ntanattcct gtnaatcgga aaatnatnt tcnncnggaa aatnttgctc ccatccgnaa 240  
 attnctccc ggtagtgc atntnggggn cngccangtt tcccaggtg ctanaatcgt 300  
 actaaagnt naagtgggan tncaaatgaa aacctnncac agagnatccn taccgactg 360  
 tnnnttncct tcgcccctng actctgcng agcccaatac ccnngngnat gtcncccnng 420  
 nnnngcgnnc tgaaannnc tcngggctnn gancatcang gggtttcgca tcaaaagcnn 480  
 cgttctncat naaggcact tngcctcacc caaccnctng cctcnncca tttngccgtc 540  
 nggttncct acgctnntng cncctnnntn ganatttnc ccgcctnggg naancctcct 600  
 gnaatgggta gggnccttnc ttttnaccnn gnggtntact aatcnnctnc acgcntnctt 660  
 tctnaccccc ccccttttt caatcccanc ggcaaatggg gtctcccnn cgangggggg 720  
 nnnccannnc c 731

<210> 29  
 <211> 822  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(822)  
 <223> n = A,T,C or G

<400> 29  
 actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60  
 cgctcanacc tcacancctc ccnaccnangc ctataangaa nannaataga nctgtncnnt 120  
 atntntacnc tcatannect cnnnaccacac tccctcttaa ccntactgt gcctatngcn 180  
 tnnctantct ntgcgcctn cnanccaccn gtggggccnac cncnngnatt ctcnatctcc 240  
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300  
 tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc 360  
 tactctgact cccacngcct annnattagc anentcccc nacnatntct caaccaaate 420  
 ntcaacaacc tatctanctg ttcnccaacc nttncctcgy atcccennac aacccccctc 480  
 ccaaataccc nccacctgac ncctaaccn caccatcccg gcaagccnan ggncatttan 540  
 ccactggaat cacnatngga naaaaaaac ccnaactctc tancncnnat ctccctaana 600  
 aatnctcctn naatttactn ncantnccat caanccacn tgaaacnaa cccctgtttt 660  
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccnctnc 720  
 ccnaatgaag gncnccaat cnangaaacg nccntgaaaa ancnaggcna anannntcgy 780  
 canatcctat cccttanttn ggggnccctt nccnngggcc cc 822

<210> 30  
 <211> 787  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(787)  
 <223> n = A,T,C or G

<400> 30  
 cggcgccctg ctctggcaca tgccctcctga atggcatcaa aagtgatgga ctgcccattg 60  
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctccccctt 120  
 gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180  
 gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240  
 acaccagggg ctccaggcag cccattattc ccagnangac atgggtgttc tccacgcgga 300  
 cccatggggc ctgnaaggcc agggctcctt ttgacaccat ctctcccgtc ctgctggca 360  
 ggccgtggga tccactantt ctanaacggn cgcaccncg gtgggagctc cagcttttgt 420  
 tccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480  
 gtgaaattgt ttntccccctc ncnattccnc ncnacatacn aaccgggaan cataaagtgt 540  
 taaagcctgg gggtngcctn nngaanaac tnaactcaat taattgcgtt ggctcatggc 600  
 ccgctttccn ttcnggaaaa ctgtcntccc ctgcnttntt gaatcggcca ccccccnggg 660  
 aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan cctnccgct 720  
 cggtcgttnc nggtngcggg gaangggnat nnnctccnc naagggggng agnnngntat 780  
 ccccaaa 787

<210> 31  
 <211> 799  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(799)  
 <223> n = A,T,C or G

<400> 31

```

tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac      60
catgtaccag ggctattaga agcaagaagg aaggaggagg ggcagagcgc cctgctgagc      120
aacaaaggac tectgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct      180
cccgcagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg      240
gtggctggtg cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca      300
ggggaccttc tgttctccca nggnaacttc nttnatctcn aaagaacaca actgtttctt      360
cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttggtaca      420
tatggttccg gcccaactct cccntcnaaa aagtaattca ccccccccn cctctnttg      480
cctgggccct taantaccca caccggaact canttantta ttcattctng gntgggcttg      540
ntnatcnccn cctgaangcg ccaagttgaa aggccacgcc gtncccnctc cccatagnan      600
nttttnnccn canctaatac cccccnngc aacnatccaa tcccccccn tgggggcccc      660
agccanggc ccccgntctg gggnnccnng cncgnantcc ccaggntctc ccantcngnc      720
ccnnngncc cccgcacgca gaacanaagg ntngagcenc cgcannnnnn nggtnnncac      780
ctgcccccc cccnccgng

```

```

<210> 32
<211> 789
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (789)
<223> n = A,T,C or G

```

```

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
ttttnccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac      120
ggcaacaggc tccggcgcg gcggcgggcg cctacctgc ggtaccaaat ntgcagcctc      180
cgctcccgtc tgatnttcct ctgcagctgc aggatgccnt aaaacagggc ctggccntn      240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc      300
nattaggaat agtggnttta cccnccnccg ttggcncact cccnttgaa accacttntc      360
gcggctccgc catctggtct taaacctgc aaacnctggg gccctctttt tggttantnt      420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancc ccccaaaacc      480
ggncatgtc ttncgggggt tgctgcnatn tncatcacct cccgggcncn ncaggncaac      540
ccaaaagtc ttngggcccn caaaaaanct ccggggggnc ccagtttcaa caaagtcatc      600
ccccttggcc cccaaatcct cccccgntt nctgggttg ggaaccacg cctctnnctt      660
tggngggcaa gntggntccc ccttcgggcc cccggtgggc ccnctctaa ngaaaacncc      720
ntcctnnnca ccatcccccc nngnnaacgnc tancaangna tccctttttt tanaaacggg      780
ccccccncc

```

```

<210> 33
<211> 793
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (793)
<223> n = A,T,C or G

```

```

<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg      60
aattcatggc tgttgagca atanaacccc agttctacga gctgctgatc aaaggacttg      120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana      180
agaagtttgc agatgtatth gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg      240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttgttcat catgatcaca      300
acaangaacg gggctcgtht atcaccantg aggagcagga cgtgagcccc cgccctgcac      360

```



```

ctctgctgtt aaacacccca gccatccctt ctttcaaaag ggatccacta cttctagagc 420
ggncgccacc gcggtggagc tccagctttt gttcccttta gtgagggtta attgcgcgct 480
tggcgtaatc atgggtcatan ctgtttcctg tgtgaaattg ttatccgctc acaattccac 540
acaacatacg anccggaagc atnaaatttt aaagcctggn ggtngcctaa tgantgaact 600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt 660
gccagctgcc nttaatgaat cnggccaccc cccggggaaa aggcngtttg cttnttgggg 720
cgcncttccc gctttctcgc ttcttgaant ccttccccc ggctcttcgg cttgcggcna 780
acggtatcna cct 793

```

```

<210> 34
<211> 756
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(756)
<223> n = A,T,C or G

```

```

<400> 34
gccgcgaccg gcatgtacga gcaactcaag ggcgagtggg accgtaaaag ccccaatctt 60
ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg 120
ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgta catactggag 180
atcggggccc aatggagcat cctacgcaan gacatccctt ccttcgagcg ctacatggcc 240
cagctcaaat gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac 300
cagctcttgg gcctcaacct cctcttcctg ctgtcccaga accgggtggc tgantnccac 360
acgganttgg ancggtgcg tgcceaanga catacanacc aatgtctaca tcnaccacca 420
gtgtcctgga gcaatactga tgganggcag ctaccncaa gtnttccttg ccnagggtaa 480
catccccgc cgagagctac accttcttca ttgacatcct gctcgacact atcagggatg 540
aaaatcgcn ggttgcctca gaaaggctnc aanaanatcc ttttcnctga aggcctccgg 600
atncnctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttncct 660
ttactgaggg ttnattgccg cccttgccgt tatcatggtc acncngttn cctgtgttga 720
aattnttaac cccccacaat tccacgcna cattng 756

```

```

<210> 35
<211> 834
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(834)
<223> n = A,T,C or G

```

```

<400> 35
ggggatctct anatcnacct gnatgcatgg ttgtcggtgt ggtcgctgtc gatgaanatg 60
aacaggatct tgccttgaa gctctcggt gctgtnttta agttgctcag tctgccgtca 120
tagtcagaca cncctctggg caaaaaacan caggatntga gtcttgattt cacctccaat 180
aatcttcngg gctgtctgct cgggtgaactc gatgacnang ggcagctggt tgtgtntgat 240
aaantccanc angttctcct tggtagctc cccttcaaag ttgttcggc cttcatcaaa 300
cttctnnaan angannanc canctttgtc gagctggnat ttgganaaca cgtcactgtt 360
ggaaactgat cccaaatggg atgtcatcca tcgctctgc tgcccgcaa aaacttgctt 420
ggcncaaate cgactcccn tccttgaaag aagccnatca cccccctc cctggactcc 480
nncaangact ctncgctnc ccntccng cagggttggg ggcancccg gccntgcgc 540
ttcttcagcc agttcacnat nttcatcagc ccctctgcca gctgtntat tccttggggg 600
ggaanccgct tctcccttcc tgaannaact ttgaccgtng gaatagccgc gcntcncnt 660
acntnctggg ccgggttcaa antccctcn ttgncntcn cctcgggcca ttctggattt 720
nccnaacttt ttccttcccc cncctcngg ngtttggntt tttcatnggg ccccaactct 780

```

gctnttggcc antccctgg gggcntntan cccccctnt ggtccctng ggcc 834

<210> 36  
 <211> 814  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(814)  
 <223> n = A,T,C or G

<400> 36  
 cggnccgttt cngccgcgc cccgtttcca tgacnaaggc tcccttcang ttaaatacnn 60  
 cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgcca 120  
 naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggctctcc acccctgta 180  
 ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact 240  
 aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca 300  
 ctaaaacanc ccagcgctca cttctgcttg ganaaatatt ctttgctctt ttggacatca 360  
 ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420  
 antgancctg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480  
 aggggagtc nttncagtg gatctgcaa anantaccn tatcatcnn gaataaaaag 540  
 gccctgaac ganatgcttc cancanctt taagacccat aatcctngaa ccattggtgcc 600  
 ctcccggtct gatccnaaag gaatgttctt ggggtccant cctcctttg ttncttacgt 660  
 tgnttggac cntgtctgn atnaccaan tganatcccc ngaagcacc tncctctggc 720  
 atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcncnaa 780  
 ggngaactca agaaggtctn ngaaaaacca cncn 814

<210> 37  
 <211> 760  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(760)  
 <223> n = A,T,C or G

<400> 37  
 gcatgctgct ctctctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60  
 gcgcagtggt cgctgaaggg gttgtagtac cagcgcgga tgctctcctt gcagagtcct 120  
 gtgtctggca ggtccacgca atgccctttg tctactggga aatggatgag ctggagctcg 180  
 tcnaanccac tcgtgtattt ttacangca gcctcctccg aagcntccg gcagttggg 240  
 gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300  
 gggctgacag gtgccagaac acactggatn ggcctttcca tggaaaggcc tgggggaaat 360  
 cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctagaaatgc 420  
 actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aacccaaanc 480  
 ttgcaaaatc tgctccgtgg gggatcatnn taccanggtt ggggaaanaa acccgcnng 540  
 gancncctt gtttgaatgc naaggnaata atcctcctgt ctgcttggg tggaaagca 600  
 caattgaact gttaacnttg ggccnggttc cncctnggtg gtctgaaact aatcacgctc 660  
 actggaaaaa ggtangtgcc ttccttgaat tcccaaanct cccctngntt tgggtnttt 720  
 ctctctncc ctaaaaatcg tnttcccccc cntanggcg 760

<210> 38  
 <211> 724  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(724)  
 <223> n = A,T,C or G

<400> 38  
 tttttttttt tttttttttt tttttttttt ttttttaaaa cccctccat tgaatgaaaa 60  
 cttccnaaat tgtccaaccc cctcnnccaa atnnccattt ccgggggggg gttccaaacc 120  
 caaattaatt ttgganttta aattaaatnt tnattnnggg aanaanccaa atgtnaagaa 180  
 aatttaaccc attatnaact taaatncctn gaaacccntg gnttccaaaa atttttaacc 240  
 cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300  
 ngatttaaac ccccttnant tnttttnacc cnngnctnaa ntatttngnt tccggtgttt 360  
 tctnttaan cntnggtaac tcccgntaat gaannnccct aanccaatta aaccgaattt 420  
 tttttgaatt ggaaattccn ngggaattna ccgggggttt tccnttttg ggcccatncc 480  
 cccnctttcg ggggtttgggn ntaggttgaa ttttttnang nccccaaaaa ncccccaana 540  
 aaaaaactcc caagnnttaa ttngaantnc ccccttccca ggcttttttg gaaaggnggg 600  
 tttntggggg ccngggantt cnttccccn ttncncccc cccccnggt aaanggttat 660  
 ngnntttggt ttttgggcc cttnanggac ctccggatn gaaattaaat ccccggnccg 720  
 gccg 724

<210> 39  
 <211> 751  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(751)  
 <223> n = A,T,C or G

<400> 39  
 tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60  
 caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120  
 tttatttatt tttactgaaa gtgagaggga acttttgttg ccttttttcc tttttctgta 180  
 ggccgcctta agctttctaa atttgaaca tctaagcaag ctgaanggaa aaggggggtt 240  
 cgcaaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300  
 ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc ttttaattana 360  
 cttgggggtt cctccccan accaaccnccn ctgacaaaaa gtgccngccc tcaaatanatg 420  
 tcccgcnnt cnttgaaca cacngcngaa ngttctcatt ntcccnccn caggtnaaaa 480  
 tgaagggtta ccatntttaa cnccacctcc acntggcnnn gcctgaatcc tcnaaaancn 540  
 cctcaancn aattnctnng ccccggtenc gentnngtcc cncccggtc ccgggaantn 600  
 cccccenga anncnntnnc naacnaaatt ccgaaaatat tccnntcnc tcaattcccc 660  
 cnnagactnt cctcnncnnc cncaattttc ttttnntcac gaacnngnnc cnnaaatgn 720  
 nnnncnctc cncnngtcn naatcnccan c 751

<210> 40  
 <211> 753  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(753)  
 <223> n = A,T,C or G

<400> 40  
 gtggtatttt ctgtaagatc aggtgttcc cctcgtagg tttagaggaa acaccctcat 60  
 agatgaaaac cccccgaga cagcagcact gcaactgcca agcagccggg gtagggggg 120

```

cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa      180
tggtctggaa gcggcggtg tacctgcgta ggggcacacc gtcagggcc accaggaact      240
tctcaaagtt ccaggcaacn tcgttcgac acaccggaga ccaggatn agcttgggt      300
cggtcataa cgcggtggcg tcgtcgtg gagctggcag ggccctccgc aggaaggcna      360
ataaaagggt cgccccgca ccgttcacct cgcacttctc naanaccatg angttgggt      420
cnaaccacc accannccg acttcctga nggaattccc aaatctctc gntcttgggc      480
ttctnctgat gccctanctg gttgccnngn atgccaanca nccccaancc ccgggggtcct      540
aaanacccn cctcctcntt tcctctgggt tntntcccc ggacctggt tcctctcaag      600
ggancccata tctcnaccan tactcacnt nccccccnt gnnaccanc cttctanngn      660
ttccncccg ncctctggcc cntcaaanan gcttnacna cctgggtctg ccttcccccc      720
tnccctatct gnacccnctn tttgtctcan tnt                                     753

```

```

<210> 41
<211> 341
<212> DNA
<213> Homo sapien

```

```

<400> 41
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt      60
agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac      120
ttctttaaac ctgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt      180
tatagtctgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag      240
tgtaaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat      300
ttttactttt tgattaattg tgttttatat attagggtag t                                     341

```

```

<210> 42
<211> 101
<212> DNA
<213> Homo sapien

```

```

<400> 42
acttactgaa tttagtctg tgctcttctt tatttagtgt tgtatcataa atactttgat      60
gtttcaaaca ttctaaataa ataattttca gtggcttcat a                                     101

```

```

<210> 43
<211> 305
<212> DNA
<213> Homo sapien

```

```

<400> 43
acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttctg gtcctcacc      60
tccagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat      120
tcagatgcct tgctaagtct agagttctag agttatgtt cagaaagtct aagaaaccca      180
cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat      240
tggatacaga acgagagtta tcctggataa ctcagagctg agtacctgcc cgggggccgc      300
tcgaa                                     305

```

```

<210> 44
<211> 852
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(852)
<223> n = A,T,C or G

```

```

<400> 44

```

```

acataaatat cagagaaaag tagtctttga aatattttacg tccaggaggt ctttgtttct 60
gattatattg tgtgtgtttt ggtttggtgc caaagtattg gcagcttcag ttttcatttt 120
ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
ccagaatttc tctttttag tagtatctca tagctcggct gagcttttca taggtcatgc 240
tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300
agacgccctc agatcgggtc tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360
ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttggtgtggc 420
acttggcagg ggggtcttgc tcctttttca tatcagggtga ctctgcaaca ggaaggtgac 480
tggtggttgt catggagatc tgagcccggc agaaagtatt gctgtccaac aaatctactg 540
tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600
gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc 660
actggccgtt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccctg 720
ccgcccgggt gaactcctgc aaactcatgc tgcaaagggt ctcgccgttg atgtcgaact 780
cntggaaagg gatacaattg gcatccagct gggtggtgtc caggaggtga tggagccact 840
cccacacctg gt 852

```

```

<210> 45
<211> 234
<212> DNA
<213> Homo sapien

```

```

<400> 45
acaacagacc cttgctcgtc aacgacctca tgctcatcaa gttggacgaa tccgtgtccg 60
agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcg gggaactcct 120
gcctcgtttc tggctgggggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg 180
tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgaccg ctgt 234

```

```

<210> 46
<211> 590
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (590)
<223> n = A,T,C or G

```

```

<400> 46
actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta 60
atttgatagc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa 120
aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa 180
tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta 240
aaagctttca aaanaanaaa ttattgcagt ctanttaatt caaacagtgt taaatggtat 300
caggataaan aactgaaggg canaaagaat taattttcac ttcattgtaac ncacccanat 360
ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aagggtctttc 420
tggtctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag 480
ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct 540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

```

```

<210> 47
<211> 774
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (774)
<223> n = A,T,C or G

```

```

<400> 47
acaagggggc ataatgaagg agtggggana gattttaaag aaggaaaaaa aacgaggccc      60
tgaacagaat tttcctgnac aacggggcctt caaaataatt ttcttgggga ggttcaagac      120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg      180
cattacagac gggactctgg gaggaaggat aaacagaaag gggacaaagg ctaatcccaa      240
aacatcaaag aaaggaagggt ggcgtcatac ctcccagcct acacagttct ccagggtctt      300
cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg      360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgat cctgcgtggc      420
ccacactcct tgaacacaca tccccaggtt atattcctgg acatggctga acctcctatt      480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc      540
acggcatggg aagcctttct gacttgccctg attactccag catcttgga caatccctga      600
ttccccactc cttagaggca agataggggtg gttaagagta gggctggacc acttgagacc      660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct      720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt          774

```

```

<210> 48
<211> 124
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (124)
<223> n = A,T,C or G

```

```

<400> 48
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt      60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact      120
tggt                                             124

```

```

<210> 49
<211> 147
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (147)
<223> n = A,T,C or G

```

```

<400> 49
gccgatgcta ctattttatt gcaggagggtg ggggtgtttt tattattctc tcaacagctt      60
tgtggctaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt      120
ttagggcacc catatcccaa gcantgt                    147

```

```

<210> 50
<211> 107
<212> DNA
<213> Homo sapien

```

```

<400> 50
acattaaatt aataaaagga ctgttgggggt tctgctaaaa cacatggcctt gatatatattgc      60
atgggtttgag gttaggagga gttaggcata tgttttggga gaggggt                    107

```

```

<210> 51
<211> 204
<212> DNA

```

<213> Homo sapien

<400> 51

gtcctaggaa	gtctagggga	cacacgactc	tggggtcacg	gggccgacac	acttgcaagg	60
cggaaggaa	aggcagagaa	gtgacaccgt	cagggggaaa	tgacagaaag	gaaaatcaag	120
gccttgcaag	gtcagaaagg	ggactcaggg	cttcaccac	agccctgccc	cacttgcca	180
cctccctttt	gggaccagca	atgt				204

<210> 52

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(491)

<223> n = A,T,C or G

<400> 52

acaaagataa	catttatctt	ataacaaaaa	tttgatagtt	ttaaaggtta	gtattgtgta	60
gggtattttc	caaaaagacta	aagagataac	tcaggtaaaa	agttagaaat	gtataaaaca	120
ccatcagaca	ggttttttaa	aaacaacata	ttacaaaatt	agacaatcat	ccttaaaaaa	180
aaaacttctt	gtatcaattt	cttttgttca	aaatgactga	cttaantatt	tttaaatttt	240
tcanaaacac	ttcctcaaaa	attttcaana	tggtagcttt	canatgtnc	ctcagtccca	300
atgttgctca	gataaataaa	tctcgtgaga	acttaccacc	caccacaagc	tttctggggc	360
atgcaacagt	gtcttttctt	tnctttttct	tttttttttt	ttacaggcac	agaaactcat	420
caattttatt	tgataaaca	agggctctcca	aatttatattg	aaaaataaat	ccaagttaat	480
atcactcttg	t					491

<210> 53

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(484)

<223> n = A,T,C or G

<400> 53

acataattta	gcagggctaa	ttaccataag	atgctattta	ttaanaggtn	tatgatctga	60
gtattaacag	ttgctgaagt	ttggattttt	tatgcagcat	tttctttttg	ctttgataac	120
actacagaac	ccttaaggac	actgaaaatt	agtaagtaaa	gttcagaaac	attagctgct	180
caatcaaatc	tctacataac	actatagtaa	ttaaaacggt	aaaaaaaaag	gttgaaatct	240
gcactagtat	anaccgctcc	tgtcaggata	anactgcttt	ggaacagaaa	gggaaaaanc	300
agctttgant	ttctttgtgc	tgatangagg	aaaggctgaa	ttaccttggt	gcctctccct	360
aatgattggc	aggtcnggta	aatnccaaaa	catattccaa	ctcaacactt	cttttccncg	420
tancttgant	ctgtgtattc	caggancagg	cggatggaat	gggccagccc	ncggatgttc	480
cant						484

<210> 54

<211> 151

<212> DNA

<213> Homo sapien

<400> 54

actaaacctc	gtgcttggtga	actccatata	gaaaacgggtg	ccatccctga	acacggctgg	60
ccactgggta	tactgctgac	aaccgcaaca	acaaaaacac	aaatccttgg	cactggctag	120

tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55  
<211> 91  
<212> DNA  
<213> Homo sapien

<400> 55  
acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60  
gccctccagt ggatactga gccaaagtgg t 91

<210> 56  
<211> 133  
<212> DNA  
<213> Homo sapien

<400> 56  
ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60  
tggaattttg gtatctgtgg gttgggggga cgggtccagga accaataccc catggatacc 120  
aagggacaac tgt 133

<210> 57  
<211> 147  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(147)  
<223> n = A,T,C or G

<400> 57  
actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60  
gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120  
tctcantggg ctggatncat gcagggt 147

<210> 58  
<211> 198  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(198)  
<223> n = A,T,C or G

<400> 58  
acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60  
tgattacata catttatcct ttaaaaaaga tgtaaacttt aatttttatg ccatctatta 120  
attaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180  
ttgacttcta agtttggt 198

<210> 59  
<211> 330  
<212> DNA  
<213> Homo sapien

<400> 59



```

acaacaaatg ggttgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat    60
ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt    120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa    180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagacccag    240
cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt    300
tttcgtcttt attggacttc tttgaagagt                                330

```

```

<210> 60
<211> 175
<212> DNA
<213> Homo sapien

```

```

<400> 60
accgtgggtg ccttctacat tcttgacggc tccttcacca acatctgggt ctacttcggc    60
gtcgtgggct ccttctctct catctctatc cagctgggtg tgctcatcga ctttgccgac    120
tcctggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctggt         175

```

```

<210> 61
<211> 154
<212> DNA
<213> Homo sapien

```

```

<400> 61
acccactttt tctcctgtg agcagtctgg acttctcact gctacatgat gagggtgagt    60
ggttggtgct cttcaacagt atcctccctt ttccggatct gctgagccgg acagcagtgc    120
tggaactgcac agccccgggg ctccacattg ctgt                                154

```

```

<210> 62
<211> 30
<212> DNA
<213> Homo sapien

```

```

<400> 62
cgctcgagcc ctatagttag tcgtattaga                                30

```

```

<210> 63
<211> 89
<212> DNA
<213> Homo sapien

```

```

<400> 63
acaagtcatt tcagaccct ttgctcttca aaactgacca tcttttatat ttaatgttc    60
ctgtatgaat aaaaatgggt atgtcaagt                                89

```

```

<210> 64
<211> 97
<212> DNA
<213> Homo sapien

```

```

<400> 64
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag    60
aatcagtgca tccaggattg gtccttgat ctggggg                                97

```

```

<210> 65
<211> 377
<212> DNA
<213> Homo sapien

```

<220>  
 <221> misc\_feature  
 <222> (1) ... (377)  
 <223> n = A,T,C or G

<400> 65  
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt tttgatggca 60  
 gcatggcgtc ctaggccttg acacagcggc tgggggtttg gctntcccaa accgcacacc 120  
 ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggg 180  
 tcggtcataa natgaaatcc caanggggac agaggctcagt agaggaagct caatgagaaa 240  
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300  
 tgggggtgaa ctaccccccag gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360  
 gggcgggagg agcatgt 377

<210> 66  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 66  
 acgcctttcc ctccagaattc agggaagaga ctgtcgcctg ccttcctccg ttgttgctg 60  
 agaaccctgt tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120  
 aggaactaac tgcaccctgg tcctctcccc agtccccagt tcaccctcca tccctcacct 180  
 tcctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240  
 ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300  
 tgttt 305

<210> 67  
 <211> 385  
 <212> DNA  
 <213> Homo sapien

<400> 67  
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60  
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120  
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180  
 tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tctttagagg 240  
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300  
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgccatac 360  
 catagtttct gtgctagtgg accgt 385

<210> 68  
 <211> 73  
 <212> DNA  
 <213> Homo sapien

<400> 68  
 acttaaccag atatatTTTT accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60  
 gtttttttaa tgg 73

<210> 69  
 <211> 536  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (536)

<223> n = A,T,C or G

<400> 69

actagtcag	tgtggtgaa	ttccattgt	ttgggggctc	tcaccctect	ctcctgcagc	60
tccagctttg	tgtctgcct	ctgaggagac	catggcccag	catctgagta	ccctgctgct	120
cctgctggcc	accctagctg	tggccctggc	ctggagcccc	aaggaggagg	ataggataat	180
ccgggtggc	atctataacg	cagacctcaa	tgatgagtgg	gtacagcgtg	cccttcactt	240
cgccatcagc	gagtataaca	aggccaccaa	agatgactac	tacagacgtc	cgctgcgggt	300
actaagagcc	aggcaacaga	ccgttggggg	ggtgaattac	ttcttcgacg	tagaggtggg	360
ccgaaccata	tgtaccaagt	cccagcccaa	cttggacacc	tgtgccttcc	atgaacagcc	420
agaactgcag	aagaaacagt	tgtgctcttt	cgagatctac	gaagtccct	ggggagaaca	480
gaangtcct	gggtgaaatc	caggtgtcaa	gaaatcttan	ggatctgttg	ccaggc	536

<210> 70

<211> 477

<212> DNA

<213> Homo sapien

<400> 70

atgacccta	acagggggcc	tctcagccct	cctaatagacc	tccggcctag	ccatgtgatt	60
tcacttccac	tccataacgc	tcctcatact	aggcctaacta	accaacacac	taaccatata	120
ccaatgatgg	cgcgatgtaa	cacgagaaag	cacataccaa	ggccaccaca	caccacctgt	180
ccaaaaaggc	cttcgatacg	ggataatcct	atttattacc	tcagaagttt	ttttcttcgc	240
agggattttt	ctgagccttt	taccactcca	gcctagcccc	taccccccaa	ctaggagggc	300
actggccccc	aacaggcatc	accccgctaa	atcccctaga	agtcccactc	ctaaacacat	360
ccgtattact	cgcatcagga	gtatcaatca	cctgagctca	ccatagtcta	atagaaaaca	420
accgaaacca	aattattcaa	agcactgctt	attacaattt	tactgggtct	ctatttt	477

<210> 71

<211> 533

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (533)

<223> n = A,T,C or G

<400> 71

agagctatag	gtacagtgtg	atctcagctt	tgcaaacaca	ttttctacat	agatagtact	60
aggatattaat	agatatgtaa	agaaagaaat	cacaccatta	ataatggtaa	gattgggtta	120
tgtgatttta	gtggtatttt	tggcaccctt	atatatgttt	tccaaacttt	cagcagtgat	180
attattttcca	taacttaaaa	agtgagttag	aaaaagaaaa	tctccagcaa	gcatctcatt	240
taaataaagg	tttgtcatct	ttaaaaatac	agcaatatgt	gactttttta	aaaagctgtc	300
aaatagggtgt	gaccctaacta	ataattatta	gaaatacatt	taaaaacatc	gagtacctca	360
agtcagttag	ccttgaaaaa	tatcaaatat	aactcttaga	gaaatgtaca	taaaagaatg	420
cttcgtaatt	ttggagtang	aggttccctc	ctcaattttg	tattttttaa	aagtacatgg	480
taaaaaaaaa	aattcacac	agtatataag	gctgtaaaaat	gaagaattct	gcc	533

<210> 72

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (511)

<223> n = A,T,C or G

```

<400> 72
tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta      60
aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa      120
aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga      180
aaacatggan agattggtgc tgganacgc cgtggctatt cctcattggt attaccanagt      240
gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca      300
cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac      360
gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg      420
atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggt atgatggcna      480
aaatacacc cctcttgaag naccnggagg a                                     511

```

```

<210> 73
<211> 499
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (499)
<223> n = A,T,C or G

```

```

<400> 73
cagtgccagc actggtgccg gtaccagtag caataacagt gccagtgccg gtgccagcac      60
cagtgtggc ttcagtgtg gtgccagcct gaccgccact ctcacatttg ggctcttcgc      120
tggccttggg ggagctggg ccagcaccag tggcagctct ggtgcctgtg gtttctccta      180
caagtgaagt tttagatatt gttaatcctg ccagtcttct tcttcaagcc aggggtgcac      240
ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca      300
ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaagg cggccgctcg      360
antctagagg gcccgtttta acccgctgat cagcctcgac tgtgccttct anttgccagc      420
catctgttgt ttgcccctcc cccgntgcct tcttgaccc tggaaagtgc cactccact      480
gtcctttcct aantaaat                                     499

```

```

<210> 74
<211> 537
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (537)
<223> n = A,T,C or G

```

```

<400> 74
tttcatagga gaacacactg aggagatact tgaagaatth ggattcagcc gcgaagagat      60
ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact      120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa      180
cattgtatgc atggaaacat ggaggaacag tattacagtg tctaccact ctaatcaaga      240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag      300
ggcttttgat ttataanaact ttgggtactt atactaaatt atggtagtta tactgccttc      360
cagtttgctt gatataattg ttgatattaa gattcttgac ttatatattg aatgggttct      420
actgaaaaan gaatgatata ttcttgaaga catcgatata cattttattt cactcttgat      480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt      537

```

```

<210> 75
<211> 467
<212> DNA
<213> Homo sapien

```

<220>  
 <221> misc\_feature  
 <222> (1)...(467)  
 <223> n = A,T,C or G

<400> 75  
 caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60  
 tgcataattac acgtacctcc tctgtctcct caagtagtgt ggtctatttt gccatcatca 120  
 cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180  
 tggcacaagg aggccatctt ttctctcatcg gttattgtcc ctgaagcgt cttctgagga 240  
 tctagttggg ctttctttct gggtttgggc catttcantt ctcagtgtgt tactattcta 300  
 tcattattgt ataacgggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360  
 caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420  
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76  
 <211> 400  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(400)  
 <223> n = A,T,C or G

<400> 76  
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcgtac 60  
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120  
 atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180  
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240  
 acttgtcttt cagcaaggac tggctcttct atctcttgta ctacactgaa ttcaccccca 300  
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360  
 ttnagtggga teganacatg taagcagcan catgggaggt 400

<210> 77  
 <211> 248  
 <212> DNA  
 <213> Homo sapien

<400> 77  
 ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60  
 ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgtgtc 120  
 caggcactgt tcattctcagc ttttctgtcc ctttgtctcc ggcaagcgt tctgtgtaa 180  
 gttcatatct ggagcctgat gtcttaacga ataaaggctc catgctccac ccgaaaaaaa 240  
 aaaaaaaa 248

<210> 78  
 <211> 201  
 <212> DNA  
 <213> Homo sapien

<400> 78  
 actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60  
 tcaccagac cccgccttgc ccgtgcccac cgctgtgtgt aacgacagta tgatgcttac 120  
 tctgtactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct 180  
 gatttaaaaa aaaaaaaaaa a 201

<210> 79  
 <211> 552  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(552)  
 <223> n = A,T,C or G

<400> 79  
 tcctttttgtt aggttttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60  
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120  
 cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180  
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240  
 atgcaagtta gtaattactc aggggttaact aaattacttt aatatgctgt tgaacctact 300  
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360  
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tgggaatttta 420  
 ttcccaggaa tatgggggttc atttatgaat antaccggg anagaagttt tgantnaaac 480  
 cngttttggt taatacgta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540  
 aaaaaaaaaa aa 552

<210> 80  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(476)  
 <223> n = A,T,C or G

<400> 80  
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60  
 ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120  
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180  
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtacta 240  
 aggttaaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300  
 tcttctaagt cctcttcag cctcactttg agtctcctt gggggttgat aggaantntc 360  
 tcttggttt ctcaataaaa tctctatcca tctcatgtt aatttggtac gcntaaaaat 420  
 gctgaaaaaa ttaaatgtt ctggtttcnc tttaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81  
 <211> 232  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(232)  
 <223> n = A,T,C or G

<400> 81  
 tttttttttg tatgcctcn ctgtggngtt attgttgctg ccaccctgga ggagcccagt 60  
 ttcttctgta tttttcttt ctgggggatc ttcttggtc tgccctcca tcccagcct 120  
 ctcatccca tcttgactt ttgctagggt tggaggcgt ttctggttag cccctcagag 180  
 actcagtcag cgggaataag tctaggggt ggggggtgtg gcaagccgc ct 232

<210> 82  
 <211> 383  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(383)  
 <223> n = A,T,C or G

<400> 82  
 aggcgggagc agaagctaaa gccaaagccc aagaagagtgc gcagtgccag cactggtgcc 60  
 agtaccagta ccaataacat gccagtgccca gtgccagcac cagtgggtggc ttcagtgtctg 120  
 gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctgggtg 180  
 ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgcgat tttagatatt 240  
 gttaatectg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300  
 agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360  
 ccatttcaaa aaaaaaaaaa aaa 383

<210> 83  
 <211> 494  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(494)  
 <223> n = A,T,C or G

<400> 83  
 accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca 60  
 gggagatcga gtctatacgc tgaagaaatt tgacccgatg ggacaacaga cctgctcagc 120  
 ccatcctgct cggttctccc cagatgacaa ataactctga caccgaatca ccatcaagaa 180  
 acgcttcaag gtgctcatga cccagcaacc gcgcctgtc ctctgagggt ccttaaactg 240  
 atgtcttttc tgccacctgt taccctcgg agactccgta accaaactct tcggactgtg 300  
 agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat 360  
 tatgcttgtg tgaggcaatc atgggtggcat caccatnaa gggaacacat ttganttttt 420  
 tttcncatat tttaaattac naccagaata ntccagaata aatgaattga aaaactctta 480  
 aaaaaaaaaa aaaa 494

<210> 84  
 <211> 380  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(380)  
 <223> n = A,T,C or G

<400> 84  
 gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60  
 agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120  
 gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttcttg 180  
 gcacaccctc ctggggccca ggcgggcacc tgctctctcc agtatgcaa ctggctgggtg 240  
 gtgtctgtcc tcgtcatctt cctgctcgtg gccaacatcc tgctgggtcac ttgctcattg 300  
 ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360  
 agcgttnccg cctcatccgg 380

<210> 85  
 <211> 481  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(481)  
 <223> n = A,T,C or G

<400> 85  
 gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60  
 tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca 120  
 ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg 180  
 tgtgaaagga tctccagaag gagtgctcga tcttcccac acttttgatg actttattga 240  
 gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc 300  
 ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac 360  
 ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa 420  
 aaagaacacc tcttggaagt gctngcgcgt cctcgtcctt tggtaggnngc gcntnccttt 480  
 t 481

<210> 86  
 <211> 472  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(472)  
 <223> n = A,T,C or G

<400> 86  
 aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt 60  
 acttggaana gcaacttnaa gcctggacac tgggtattaaa attcacaata tgcaacactt 120  
 taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg 180  
 ccctattcac acctgtttaa agggcgctaa gcatttttga ttcaacatct ttttttttga 240  
 cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt 300  
 catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg 360  
 atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga 420  
 tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg 472

<210> 87  
 <211> 413  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(413)  
 <223> n = A,T,C or G

<400> 87  
 agaaaccagt atctctnaaa acaacctctc ataccttggtg gacctaatTT tgtgtgcgtg 60  
 tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttTga aaagcttatg 120  
 cctctttggT atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180  
 ttgtcttctg tgtaaatggT actagagaaa acacctatnt tatgagtcaa tctagttngt 240  
 tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg 300



```

ggggacaaag aaaagcanaa ctgaacatna gaaacaattn cctggtgaga aattncataa 360
acagaaattg ggtngtatat tgaaananng catcattnaa acgttttttt ttt 413

```

```

<210> 88
<211> 448
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(448)
<223> n = A,T,C or G

```

```

<400> 88
cgcagcgggt cctctctatc tagctccagc ctctcgccgtg ccccaactccc cgcgtcccgc 60
gtcctagccn accatggccg ggcccctgcg cgccccgctg ctctctgtgg ccatcctggc 120
cgtggccctg gccgtgagcc ccgcccgcgg ctccagtcctc ggcaagccgc cgcgcctggt 180
gggaggccca tggaccccg cgtggaagaag aaggtgtgcg gcgtgcactg gactttgccg 240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc 300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng 360
tttaccagaa ccnagccaat tngaacaatt ncccctccat aacagcccct tttaaaaagg 420
gaancantcc tgntcttttc caaat ttt 448

```

```

<210> 89
<211> 463
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

```

```

<400> 89
gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60
gtagtatttc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120
agaggtctag gtctgcatac cagcagacag tttgtccgtg tattttgtag ccttgaagtt 180
ctcagtgaca agttntttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240
tttnatgttn agacttgcct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg 300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccctcnn 420
aattcnnana anttcagntn tcatacaaca naacngganc ccc 463

```

```

<210> 90
<211> 400
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

```

```

<400> 90
agggattgaa ggtctntnt actgtcggac tgttcancca ccaactctac aagttgctgt 60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaat 120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttcact 180
tcctttgtta agacttcac tggtaaaagtc ttaagttttg tagaaaggaa ttaattgct 240

```

```

cggtctctaa caatgtcttc tccttgaagt atttggctga acaaccacc tnaagtcctt    300
ttgtgcatcc attttaaata tacttaatag ggcattggtn cactaggtta aattctgcaa    360
gagtcacctg tctgcaaaag ttgcgttagt atatctgcca                        400

```

```

<210> 91
<211> 480
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (480)
<223> n = A,T,C or G

```

```

<400> 91
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact    60
ggctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac    120
atgcctcttt gactaccgtg tgccagtgtc ggtgattctc acacacctcc nccgctctt    180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaaat tcaccacga    240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt    300
tgtcaatact aaccgctggg tttgcctcca tcacatttgt gatctgtagc tctggatata    360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt    420
ngatcagggt cccatttccc agtcgcaatg ttcacatggc atatnttact tcccacaaaa    480

```

```

<210> 92
<211> 477
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (477)
<223> n = A,T,C or G

```

```

<400> 92
atacagccca natccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact    60
ggctccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt    120
cccacgcagg cagcagcggg gccggtcaat gaactccact cgtggcttgg ggttgacggt    180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccgaact gtgcgggacc    240
tgcagcgaaa ctctcgatg gtcagtagcg ggaagcgaat gangcccagg gccttgccca    300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg    360
accagcggac aaacggcggt gaacagccgc acctcacgga tgcccantgt gtgcgctcc    420
aggaacggcn ccagcgtgtc caggtcaatg tcggtgaanc ctccgcgggt aatggcg      477

```

```

<210> 93
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (377)
<223> n = A,T,C or G

```

```

<400> 93
gaacggctgg accttgcttc gcattgtgct gctggcagga ataccttggc aagcagctcc    60
agtccgagca gcccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc    120
cgcctcaatg cagaaccant agtgggagca ctgtgttagt agttaagagt gaacactgtg    180

```

tgattttact	tggaatttc	ctctgttata	tagcttttcc	caatgctaata	ttccaaacaa	240
caacaacaaa	ataacatgtt	tgctgttna	gttgataaaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaantttctg	tattttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94  
 <211> 495  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(495)  
 <223> n = A,T,C or G

<400> 94						
ccctttgagg	ggttagggtc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaccc	cagagccctg	ggctatagtc	tctgaccctt	120
ccaaggaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttcccgcag	gaggaaggga	aggggctctg	tgtgcccccc	240
acgaggaana	ggccctgant	cctgggatca	nacaccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggtccc	ctctcagttc	cttcctaca	ccctgaacgg	nacttgcccc	360
acaccacccc	agancancca	cccgccatgg	ggaatgttct	caaggaatcg	cngggcaacg	420
tggaactctng	ttccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480
aaaaaaaaana	aaaaa					495

<210> 95  
 <211> 472  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(472)  
 <223> n = A,T,C or G

<400> 95						
ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tattttattat	cttgtagaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggaacaa	tgtggagtgt	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttgggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taattttctt	ccttgttttac	gttaattttg	aaaagaatgc	at	472

<210> 96  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(476)  
 <223> n = A,T,C or G

<400> 96						
ctgaagcatt	tcttcaaact	tntctacttt	tgctcattgat	acctgtagta	agttgacaat	60

```

gtgggtgaaat ttcaaaatta tatgtaactt ctactagttt tactttctcc cccaagtctt 120
ttttaactca tgatttttac acacacaatc cagaacttat tatatagcct ctaagtcttt 180
attcttcaca gtagatgatg aaagagtcct ccagtgctct gngcanaatg ttctagntat 240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaaat 300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct 360
gcagggtact ctcagaaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt 420
tacaaagtct atcttcctca nangtctgtn aaggaacaat ttaatcttct agcttt 476

```

<210> 97

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 97

```

actctttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaatggata 60
aaataatgct gcaaaactta tgttcttatg caaaatggaa cgctaataaa acacagctta 120
caatcgcaaa tcaaaactca caagtgetca tctgtttag atttagtgtg ataagactta 180
gattgtgctc ctctggatat gattgtttct canatcttg gcaatnttcc ttagtcaaat 240
caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt 300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat 360
ntnnttttta natcaaagta ttttgtgttt ggaantgttn aaatgaaatc tgaatgtggg 420
ttcnatctta ttttttccn gacnactant tnttttttta gggncatattc tganccatc 479

```

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

```

agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcaactgaca atcagaccta 60
tgctagtctc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca 120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
agtgattcag ttctctctac ggatgagaga ctggctcaag aatatactca tgcagcttta 240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaaat 300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaggact 360
ttaagaaaaa ctaccacatg ttgtgtatcc tgggtgccgc cgtttatgaa ctgaccaccc 420
tttgaataaa tcttgacgct cctgaacttg ctccctctgcg a 461

```

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

```

gtggccgcgc gcagggtgtt cctcgtaccg cagggccccc tcccttcccc aggcgtccct 60
cggcgctct gcgggcccga ggaggagcgg ctggcgggtg gggggagtgt gaccacccct 120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c 171

```

<210> 100

<211> 269

<212> DNA

<213> Homo sapien

&lt;400&gt; 100

cggccgcaag	tgcaactcca	gctggggccg	tgccggacgaa	gattctgcc	gcagttggtc	60
cgactgcgac	gacggcggcg	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggtcgtgt	cacgtcccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggg	gaagcgggag	gcctcgggga	gcccctcggg	aagggcggcc	240
cgagagatac	gcaggtgcag	gtggccgcc				269

&lt;210&gt; 101

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 101

tttttttttt	ttttggaatc	tactgcgagc	acagcagggtc	agcaacaagt	ttattttgca	60
gctagcaagg	taacagggtg	gggcatggtt	acatgttcag	gtcaacttcc	ttgtcgtgg	120
ttgattggtt	tgtctttatg	ggggcggggt	ggggtagggg	aaacgaagca	aataacatgg	180
agtgggtgca	ccctccctgt	agaacctggt	tacaaagctt	ggggcagttc	acctggtctg	240
tgaccgtcat	tttcttgaca	tcaatgttat	tagaagtcag	gatatctttt	agagagtcca	300
ctgttctgga	gggagattag	ggtttcttgc	caaatccaac	aaaatccact	gaaaaagttg	360
gatgatcagt	acgaataccg	aggcatattc	tcatatcggt	ggcca		405

&lt;210&gt; 102

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 102

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
ggcacttaat	ccatttttat	ttcaaaatgt	ctacaaattt	aatcccattha	tacgggtattt	120
tcaaaatcta	aattattcaa	attagccaaa	tccttaccaa	ataataccca	aaaatcaaaa	180
atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atatatacgg	ctgggtgtttt	240
caaagtacaa	ttatcttaac	actgcaaaca	ttttaaggaa	ctaaaataaa	aaaaaacact	300
ccgcaaaggt	taaagggaac	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	tttactcact	ttgtttattt	420
ttttaaacca	ttgtttgggc	ccaacacaat	ggaatcccc	ctggactagt		470

&lt;210&gt; 103

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 103

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccttattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaaca	ggaagagaaa	tggcacacaa	aacaaacatt	ttatattcat	atttctacct	420
acgttaataa	aatagcattt	tgtgaagcca	gctcaaaaaga	aggcttagat	ccttttatgt	480
ccattttagt	cactaaacga	tatcaaagtg	ccagaatgca	aaaggtttgt	gaacatttat	540
tcaaaaagcta	atataagata	tttcacatac	tcattcttct	g		581

&lt;210&gt; 104

&lt;211&gt; 578

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 104

tttttttttt	tttttttttt	tttttctctt	cttttttttt	gaaatgagga	tcgagttttt	60
cactctctag	atagggcctg	aagaaaactc	atctttccag	ctttaaaata	acaatcaaat	120
ctcttatgct	atatcatatt	ttaagttaaa	ctaagttagc	actggcttat	cttctcctga	180
aggaaatctg	ttcattcttc	tcattcatat	agttatatca	agtactacct	tgcatattga	240
gagggttttc	ttctctatct	acacatatat	ttccatgtga	atttgatatca	aacctttatt	300
ttcatgcaaa	ctagaaaata	atgtttcttt	tgcataagag	aagagaacaa	tatagcatta	360
caaaactgct	caaattgttt	gttaagttaa	ccattataat	tagttggcag	gagctaatac	420
aatcacatt	tacgacagca	ataataaaac	tgaagtacca	gttaaataac	caaaaataatt	480
aaaggaacat	tttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
tgaattcaca	tggtattatt	cctagcccaa	cacaatgg			578

&lt;210&gt; 105

&lt;211&gt; 538

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 105

tttttttttt	tttttcagta	ataatcagaa	caatatattat	ttttatatatt	aaaattcata	60
gaaaagtgc	ttacatttaa	taaaagtttg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacattaag	taaaattatt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaaata	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttcttttcta	tgggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

&lt;210&gt; 106

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

tttttttttt	tttttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
atttattagc	tctgcaactt	acatatattaa	attaaagaaa	cgtttttagac	aactgtacaa	120
tttataaatg	taagggtgcc	ttattgagta	atatatttct	ccaagagtgg	atgtgtccct	180
tctccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatcccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcttc	ggtggcaaga	actcttcgaa	420
ccgtctcttc	aaaggcgctg	ccacatttgt	ggctctttgc	acttgtttca	aaa	473

&lt;210&gt; 107

&lt;211&gt; 1621

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 107

cgccatggca	ctgcagggca	tctcggtcat	ggagctgtcc	ggcctggccc	cgggcccgtt	60
ctgtgctatg	gtcctggctg	acttcggggc	gcgtgtggta	cgctgggacc	ggcccggctc	120
ccgctacgac	gtgagccgct	tgggccgggg	caagcgctcg	ctagtgtctg	acctgaagca	180
gccgcgggga	gccgccgtgc	tgccgcgtct	gtgcaagcgg	tcggatgtgc	tgctggagcc	240
cttcgccgcg	ggtgtcatgg	agaaactcca	gctgggccc	gagattctgc	agcgggaaaa	300
tccaaggctt	atttatgcca	ggctgagtg	atttgccag	tcaggaagct	tctgccggtt	360
agctggccac	gatatcaact	atttgcttt	gtcaggtgtt	ctctcaaaaa	ttggcagaag	420
tggtgagaat	ccgtatgccc	cgctgaatct	cctggctgac	tttgctggtg	gtggccttat	480
gtgtgcactg	ggcattataa	tggtcttttt	tgaccgcaca	cgactgaca	agggtcagg	540

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cattgatgca aatatggtgg aaggaacagc atatttaagt tcttttctgt ggaaaactca 600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat 780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
gaaggcagag tgggtgtcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
ttttgaggag gttgttcac atgatacaca caaggaacgg ggctcgttta tcaccagtga 960
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tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt 1080
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agctagtctc taacttccag gcccacggct caagtgaatt tgaatactgc atttacagtg 1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
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aatggttctc attagggctt ttgatttata aaactttggg tacttatact aaattatggt 1380
agttattctg ccttccagtt tgcttgatat atttggtgat attaagattc ttgacttata 1440
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atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatgggtgat 1560
aaaagtcacg tgaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
a

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&lt;210&gt; 108

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 108

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1      5      10      15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210    215    220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225    230    235    240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245    250    255

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Asn	Gln	Met	Ser	Met	Asp	Asp	Trp	Pro	Glu	Met	Lys	Lys	Lys	Phe	Ala
		260						265					270		
Asp	Val	Phe	Ala	Lys	Lys	Thr	Lys	Ala	Glu	Trp	Cys	Gln	Ile	Phe	Asp
		275					280					285			
Gly	Thr	Asp	Ala	Cys	Val	Thr	Pro	Val	Leu	Thr	Phe	Glu	Glu	Val	Val
	290					295					300				
His	His	Asp	His	Asn	Lys	Glu	Arg	Gly	Ser	Phe	Ile	Thr	Ser	Glu	Glu
305					310					315					320
Gln	Asp	Val	Ser	Pro	Arg	Pro	Ala	Pro	Leu	Leu	Leu	Asn	Thr	Pro	Ala
				325					330					335	
Ile	Pro	Ser	Phe	Lys	Arg	Asp	Pro	Phe	Ile	Gly	Glu	His	Thr	Glu	Glu
			340					345					350		
Ile	Leu	Glu	Glu	Phe	Gly	Phe	Ser	Arg	Glu	Glu	Ile	Tyr	Gln	Leu	Asn
	355					360					365				
Ser	Asp	Lys	Ile	Ile	Glu	Ser	Asn	Lys	Val	Lys	Ala	Ser	Leu		
	370					375					380				

&lt;210&gt; 109

&lt;211&gt; 1524

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 109

ggcacgaggg	tgcgccaggg	cctgagcggg	ggcgggggca	gcctcgccag	cggggggcccc	60
gggcctggcc	atgcctcact	gagccagcgc	ctgcgcctct	acctcgccga	cagctggaac	120
cagtgcgacc	tagtggtctt	cacctgcttc	ctcctgggcg	tgggctgccg	gctgaccccc	180
ggtttgtacc	acctgggccc	cactgtcctc	tgcatcgact	tcatggtttt	cacggtgcgg	240
ctgcttcaca	tcttcacggt	caacaaacag	ctggggccca	agatcgctcat	cgtgagcaag	300
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&lt;210&gt; 110

&lt;211&gt; 3410

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 110

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gtgatgagac	gtgtccccac	tgaggtgccc	cacagcagca	ggtgttgagc	atgggctgag	120



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aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaataa	aaaaaaaaaa		3410

&lt;210&gt; 111

&lt;211&gt; 1289

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 111

```

agccaggcgt ccctctgcct gcccaactcag tggcaacacc cgggagctgt tttgtccttt      60
gtggagcctc agcagttccc tctttcagaa ctcaactgcc agagccctga acaggagcca      120
ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcactcttc      180
tgtgtggtgc agccctgttg gcagtgggca tctgggtgtc aatcgatggg gcatcctttc      240
tgaagatcct cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc      300
tcacgcgacg cggcggtgtg gtctttgctc ttggtttcct gggctgctat ggtgctaaga      360
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aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc      1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa                                1289

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&lt;210&gt; 112

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1          5          10          15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
      20          25          30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
      35          40          45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
      50          55          60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
      65          70          75          80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
      85          90          95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
      100          105          110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
      115          120          125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
      130          135          140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
      145          150          155          160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
      165          170          175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
      180          185          190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

```

      195              200              205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
  210              215              220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
  225              230              235              240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
      245              250              255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
      260              265              270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
      275              280              285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
  290              295              300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
  305              310              315

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<210> 113
<211> 553
<212> PRT
<213> Homo sapien

```

```

      <400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
  1              5              10              15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
      20              25              30
Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
      35              40              45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
      50              55              60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
      65              70              75              80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
      85              90              95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
      100              105              110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
      115              120              125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
      130              135              140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
      145              150              155              160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
      165              170              175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
      180              185              190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
      195              200              205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
      210              215              220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
      225              230              235              240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
      245              250              255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
      260              265              270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
      275              280              285

```

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

&lt;210&gt; 114

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 114

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
 85 90 95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
 115 120 125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met

130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		160
	165	170
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		175
	180	185
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		190
	195	200
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		205
	210	215
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		220
225	230	235
Gln		240

<210> 115  
 <211> 366  
 <212> DNA  
 <213> Homo sapien

<400> 115  
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 catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac 120  
 ttggtttctg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180  
 actggtagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggg 240  
 tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt 300  
 tctctaatac cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360  
 ttagtc 366

<210> 116  
 <211> 282  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(282)  
 <223> n = A,T,C or G

<400> 116  
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 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120  
 agactttact attttcatat tttaagacac atgatttatc ctatttttagt aacctgggtc 180  
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240  
 tcaatctnga actatctana tcacagacat ttctattcct tt 282

<210> 117  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(305)  
 <223> n = A,T,C or G

<400> 117

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acacatgtcg cttcaactgcc ttcttagatg cttctgggtca acatanagga acagggacca      60
tatttatacct ccttcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa      120
aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga      180
tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt      240
gactgcccc gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat      300
tggggt                                           305

```

<210> 118

<211> 71

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(71)

<223> n = A,T,C or G

<400> 118

```

accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa      60
aantctggg t                                           71

```

<210> 119

<211> 212

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(212)

<223> n = A,T,C or G

<400> 119

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actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca      60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac      120
agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant      180
aatggantca aganactccc aggccctcagc gt                                           212

```

<210> 120

<211> 90

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(90)

<223> n = A,T,C or G

<400> 120

```

actcggttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctcttgcc      60
ctccgccggc gcagaacatg ctgggggtgg                                           90

```

<210> 121

<211> 218

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

&lt;222&gt; (1)...(218)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 121

tgtancgtga	anacgacaga	naggggtgtc	aaaaatggag	aanccttgaa	gtcattttga	60
gaataagatt	tgctaaaaga	tttggggcta	aaacatgggt	attgggagac	atttctgaag	120
atatncangt	aaattangga	atgaattcat	ggttcttttg	ggaattcctt	tacgatngcc	180
agcatanact	tcatgtgggg	atancagcta	cccttgta			218

&lt;210&gt; 122

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 122

taggggtgta	tgcaactgta	aggacaaaaa	ttgagactca	actggcttaa	ccaataaagg	60
catttgtag	ctcatggaac	aggaagtcgg	atgggtgggc	atcttcagtg	ctgcatgagt	120
caccaccccg	gcgggggtcat	ctgtgccaca	ggtcctgtt	gacagtgcgg	t	171

&lt;210&gt; 123

&lt;211&gt; 76

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(76)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 123

tgtagcgtga	agacnacaga	atgggtgtgtg	ctgtgctatc	caggaacaca	tttattatca	60
ttatcaanta	ttgtgt					76

&lt;210&gt; 124

&lt;211&gt; 131

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 124

acctttcccc	aaggccaatg	tectgtgtgc	taactggccg	gctgcaggac	agctgcaatt	60
caatgtgctg	ggatcatatg	aggggaggag	actctaaaat	agccaatttt	attctcttgg	120
ttaagatttg	t					131

&lt;210&gt; 125

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 125

actttatcta	ctggctatga	aatagatgg	ggaaaattgc	gttaccaact	ataccactgg	60
cttgaaaaag	aggtgatagc	tcttcagagg	acttgtgact	tttgctcaga	tgctgaagaa	120
ctacagtctg	catttggcag	aaatgaagat	gaatttggat	taaatgagga	tgctgaagat	180
ttgcctcacc	aaacaaaagt	gaaacaactg	agagaaaatt	ttcaggaaaa	aagacagtgg	240
ctcttgaagt	atcagtcact	tttgagaatg	tttcttagtt	actgcatact	tcatggatcc	300
catggtgggg	gtcttgcata	tgtaagaatg	gaattgattt	tgcttttgca	agaatctcag	360
caggaaacat	cagaaccact	atcttctagc	cctctgtcag	agcaaaccct	agtgcctctc	420
ctctttgctt	gt					432

<210> 126  
 <211> 112  
 <212> DNA  
 <213> Homo sapien

<400> 126  
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60  
 agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt 112

<210> 127  
 <211> 54  
 <212> DNA  
 <213> Homo sapien

<400> 127  
 accacgaaac cacaacaag atggaagcat caatccactt gccaagcaca gcag 54

<210> 128  
 <211> 323  
 <212> DNA  
 <213> Homo sapien

<400> 128  
 acctcattag taattgtttt gttgtttcat ttttttctaa tgttctccct ctaccagctc 60  
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120  
 ttctctctga agtctagggt acccattttg gggacccatt ataggcaata aacacagttc 180  
 ccaaagcatt tggacagttt cttgtttgtg tttagaatgg ttttcctttt tcttagcctt 240  
 ttcttgcaaa aggtcactc agtcccttgc ttgtcagtg gactgggctc cccagggcct 300  
 aggtgcctt cttttccatg tcc 323

<210> 129  
 <211> 192  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(192)  
 <223> n = A,T,C or G

<400> 129  
 acatacatgt gtgtatattt ttaaataatca cttttgtatc actctgactt tttagcatac 60  
 tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120  
 tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180  
 gataaacaaa gt 192

<210> 130  
 <211> 362  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(362)  
 <223> n = A,T,C or G

<400> 130  
 ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60



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tataatgacg caacaaaaag gtgctgttta gtcctatggg tcagtttatg cccctgacaa 120
gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa 180
ttctgtattc cattttgtta acgcctggga gatgtaacct gctangaggc taactttata 240
cttatttaaa agctcttatt ttgtggatcat taaaatggca atttatgtgc agcactttat 300
tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaacttta aaaagtaatg 360
gg 362

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<210> 131

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131

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ctttttgaaa gategtgtcc actcctgtgg acatcttggt ttaatggagt ttcccatgca 60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga 120
gttctcccag gttgcacctg ctgctccaag tctcagcagc agcctctttt aggaggcatc 180
ttctgaaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa 240
cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc 300
atanaaggat tgggtgaagc tggcgttgtg gt 332

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<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132

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acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc 60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat 120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt 180
tttagcaagt taaaatgaan atgacaggaa aggccttatt atcaacaaag agaagagttg 240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct aggggaagcct 300
gtaacaatct acaattgggc ca 322

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<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133

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acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt 60
cttgtttttc tttccatctg gtccttgggt tgacaatttg tggaaacaac tctattgcta 120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg 180
ctattcctgt ttgtcaaaag aaatttatatt tttcaaaata tgtntatttg tttgatgggt 240

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cccacgaaac actaataaaa accacagaga ccagcctg 278

<210> 134  
 <211> 121  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(121)  
 <223> n = A,T,C or G

<400> 134  
 gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca 60  
 tgattctctg aggttaaact tggttttcaa atgttatttt tacttgtatt ttgcttttgg 120  
 t 121

<210> 135  
 <211> 350  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(350)  
 <223> n = A,T,C or G

<400> 135  
 acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctatacc 60  
 atancaagtgt gtgactgggt aagcgtgcga caaagggtcag ctggcacatt acttgtgtgc 120  
 aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca 180  
 ggggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct 240  
 ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300  
 ttcccaaggga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136  
 <211> 399  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(399)  
 <223> n = A,T,C or G

<400> 136  
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60  
 gctgtgattg tatccgaata ntctcgtga gaaaagataa tgagatgacg tgagcagcct 120  
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180  
 cctggcggcc agccagccag ccacaggtgg gcttcttctt tttgtggtga caacnccaag 240  
 aaaactgcag agggccaggg tcaggtgtna gtgggtangt gaccataaaa caccaggtgc 300  
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 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137  
 <211> 165  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(165)  
 <223> n = A,T,C or G

<400> 137  
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 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120  
 ttggctggtc ccactgggtg tcaactgtcat tggggtgggt cctgt 165

<210> 138  
 <211> 338  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(338)  
 <223> n = A,T,C or G

<400> 138  
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60  
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa 120  
 tgctgggcag tctcccatgc ctccacagt gaaagggctt gagaaaaatc acatccaatg 180  
 tcatgtgttt ccagccacac caaaaggtgc ttgggggtgga gggctggggg catananggt 240  
 cangcctcag gaagcctcaa gtccattca gctttgccac tgtacattcc ccatntttaa 300  
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139  
 <211> 382  
 <212> DNA  
 <213> Homo sapien

<400> 139  
 gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60  
 gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga 120  
 attcaaacag acctcgatc tctggtgtg agcctggtcg gctcacgcc tatcatctgc 180  
 atttgcctta ctgagtgct accggactct ggccctgat gtctgtagt tcacaggatg 240  
 ccttatttgt cttctacacc ccacagggcc cctacttct tcggatgtgt ttttaataat 300  
 gtcagctatg tgecccatcc tcttcatgc cctccctccc tttcctacca ctgctgagt 360  
 gcctggaact tgtttaaagt gt 382

<210> 140  
 <211> 200  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(200)  
 <223> n = A,T,C or G

<400> 140  
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 acttttcat taacancttt tgtaagtgt caggctgcac tttgctccat anaattattg 120  
 ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt 180  
 atattcagca taaaggagaa 200

<210> 141  
<211> 335  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(335)  
<223> n = A,T,C or G

<400> 141  
actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg 60  
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttggt 120  
atgcatgtag agaaccctaa ctaatttatt aaacaggata gaaacaggct gtctgggtga 180  
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg 240  
tttttctacc agttcagaga tnggttaatg actanttcca atgggggaaaa agcaagatgg 300  
attcacaac caagtaattt taaacaaaga cactt 335

<210> 142  
<211> 459  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(459)  
<223> n = A,T,C or G

<400> 142  
accaggttta tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta 60  
gggttggtta aagacaaccc agcttaatat caagagaaat tgtgaccttt catggagtat 120  
ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180  
cacatggtcc aacaacactc aaataataaa tcaaataatna tcagatgtta aagattggtc 240  
ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca 300  
tcaaacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360  
agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420  
cagcangggg gggaggaacc agctcaacct tggcgant 459

<210> 143  
<211> 140  
<212> DNA  
<213> Homo sapien

<400> 143  
acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60  
aaatccaaac agtctctcct agaaaggaat agtgtcacca accccacca tctccctgag 120  
accatccgac ttccctgtgt 140

<210> 144  
<211> 164  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(164)  
<223> n = A,T,C or G

<400> 144  
 acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60  
 atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg 120  
 aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145

<211> 303

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 145  
 acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60  
 actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat 120  
 gcaggacagc tatcataagt cgccccaggc atccagatac taccatttgt ataaacttca 180  
 gtaggggagt ccatccaagt gacaggtcta atcaaaggag gaaatggaac ataagcccag 240  
 tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgcctggg tgattaccat 300  
 caa 303

<210> 146

<211> 327

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(327)

<223> n = A,T,C or G

<400> 146  
 actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60  
 actggcctgg agtgactcat tgctctgggt gggtgagaga gctcctttgc caacaggcct 120  
 ccaagtcagg gctgggattt gtttcccttc cacattctag caacaatatg ctggccactt 180  
 cctgaacagg gagggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240  
 agacttgccc ctgggcctgt cacacctact gatgacctc tgtgcctgca ggatggaatg 300  
 taggggtgag ctgtgtgact ctatggt 327

<210> 147

<211> 173

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(173)

<223> n = A,T,C or G

<400> 147  
 acattgtttt tttgagataa agcattgana gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattatc agttccatgt ttatagccta gtt 173

<210> 148

<211> 477  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(477)  
 <223> n = A,T,C or G

<400> 148  
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc tttctatcct 60  
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120  
 gccctactac ctgctgcaat aaacacattc ctttctgtgc ctgaccctga agccattggg 180  
 gtggctctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgtcac 240  
 nccanccac ctcaccgacc ccacccctct acacagctac ctccttgctc tctaaccaca 300  
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccg acatgtccag 360  
 caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420  
 ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atgggtgg 477

<210> 149  
 <211> 207  
 <212> DNA  
 <213> Homo sapien

<400> 149  
 acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac 60  
 taacgtatnt tagagagcca aggaaggttt ctgtggggag tgggatgtaa ggtggggcct 120  
 gatgataaat aagagtcagc caggtaagtg ggtgggtgtg tatgggcaca gtgaagaaca 180  
 tttcaggcag agggaacagc agtgaaa 207

<210> 150  
 <211> 111  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(111)  
 <223> n = A,T,C or G

<400> 150  
 accttgatnt cattgtgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60  
 cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151  
 <211> 196  
 <212> DNA  
 <213> Homo sapien

<400> 151  
 agcgcgagc gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac 60  
 agcaagatgg ctttgaactc aggtcacca ccagctattg gaccttacta tgaaaaccat 120  
 ggataccaac cggaaaaccc ctatcccgca cagccactg tgggtccacac tgtctacgag 180  
 gtgcatccgg ctgagt 196

<210> 152  
 <211> 132  
 <212> DNA

<213> Homo sapien

<400> 152

acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaag ataacagAAC	60
cttccccttt tcatctagtG gtggaaacct gatgctttat gttgacagga atagaaccag	120
gagggagttt gt	132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
cttctgtctt tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga	120
gcacatcaat aaagtccaaa gtcttggaact tggccttggc ttggaggaag tcatcaacac	180
cctggctagt gaggggtgcgg cgccgtcctt ggatgacggc atctgtgaag tctgtcacca	240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt	285

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

accacagtcc tgttggggcca gggcttcatg accctttctg tgaaaagcca tattatcacc	60
accccaaat tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac	120
cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg	180
attggcacag gagtccaagg tgttcagctc cctcctccg tggaaacgaga ctctgatttg	240
agtttcacaa attctcgggc cactcgtca ttgctcctt gaaataaaat ccggagaatg	300
gtcaggcctg tctcatccat atggatcttc cgg	333

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

actggaaata ataaaaccca catcacagtG ttgtgtcaaa gatcatcagg gcatggatgg	60
gaaagtgtt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat	120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc	180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct	240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcagtctg	300
gccctggt	308

<210> 156

<211> 295

<212> DNA

<213> Homo sapien

<400> 156

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ttattgatta	ctgagagAAC	tgtagacat	ttagttgaag	attttctaca	caggaaactga	120
gaataggaga	ttatgtttgg	ccctcatatt	ctctcctatc	ctccttgcct	cattctatgt	180
ctaataatatt	ctcaatcaaa	taaggtttagc	ataatcagga	aatcgaccaa	ataccaatat	240
aaaaccagat	gtctatcctt	aagattttca	aatagaaaac	aaattaacag	actat	295

<210> 157

<211> 126

<212> DNA

<213> Homo sapien

<400> 157

acaagtttaa	atagtgtgt	cactgtgcat	gtgctgaaat	gtgaaatcca	ccacatttct	60
gaagagcaaa	acaaattctg	tcattgtaac	tctatcttgg	gtcgtgggta	tatctgtccc	120
cttagt						126

<210> 158

<211> 442

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (442)

<223> n = A,T,C or G

<400> 158

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aanccagcag	gctgccccta	gtcagtcctt	ccttcacagag	aaaaagagat	ttgagaaagt	120
gcctgggtaa	ttcaccatta	atttcctccc	ccaaactctc	tgagtcttcc	cttaatatatt	180
ctggtgggtc	tgaccaaagc	aggtcatggt	ttgttgagca	tttgggatcc	cagtgaagta	240
natgtttgta	gccttgcata	cttagccctt	cccacgcaca	aacggagtgg	cagagtgggtg	300
ccaaccctgt	tttcccagtc	cacgtagaca	gattcacagt	gcggaattct	ggaagctgga	360
nacagacggg	ctctttgcag	agccgggact	ctgagangga	catgagggcc	tctgcctctg	420
tgttcattct	ctgatgtcct	gt				442

<210> 159

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (498)

<223> n = A,T,C or G

<400> 159

acttccaggt	aacgttggtg	tttccgttga	gcctgaactg	atgggtgacg	ttgtaggttc	60
tccaacaaga	actgaggttg	cagagcgggt	aggggaagagt	gctgttccag	ttgcacctgg	120
gctgctgtgg	actgttggtg	attcctcact	acggcccaag	gttgtggaac	tggcanaaag	180
gtgtgttggt	gganttgagc	tcgggcggct	gtggtaggtt	gtgggctctt	caacaggggc	240
tgctgtggtg	ccgggangtg	aangtggtgt	gtcacttgag	cttggccagc	tctggaaagt	300
antanattct	tcctgaaggc	cagcgcttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccaagt	ctgctgtggg	tgggtgtana	tcctccacaa	agcctgaagt	tatggtgtcn	420
tcaggttaana	atgtggtttc	agtgtccctg	ggcngctgtg	gaaggttgta	nattgtcacc	480



aagggaataa gctgtggt

498

&lt;210&gt; 160

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(380)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 160

acctgcattc	agcttcctg	ccaaactcac	aaggagacat	caacctctag	acagggaaac	60
agcttcagga	tacttccagg	agacagagcc	accagcagca	aaacaaatat	tcccatgcct	120
ggagcatggc	atagaggaag	ctganaaatg	tggggctctga	ggaagccatt	tgagtctggc	180
cactagacat	ctcatcagcc	acttgtgtga	agagatgccc	catgacccca	gatgcctctc	240
ccacccttac	ctccatctca	cacacttgag	ctttccactc	tgtataattc	taacatcctg	300
gagaaaaatg	gcagtttgac	cgaacctgtt	cacaacggta	gaggctgatt	tctaacgaaa	360
cttgtagaat	gaagcctgga					380

&lt;210&gt; 161

&lt;211&gt; 114

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 161

actccacatc	cctctgagc	aggcggttgt	cgttcaaggt	gtatttgccc	ttgcctgtca	60
cactgtccac	tggcccctta	tccacttggt	gcttaatccc	tcgaaagagc	atgt	114

&lt;210&gt; 162

&lt;211&gt; 177

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 162

actttctgaa	tcgaatcaaa	tgatacttag	tgtagtttta	atatectcat	atatatcaaa	60
gttttactac	tctgataatt	ttgtaaacca	ggtaaccaga	acatccagtc	atacagcttt	120
tggtgatata	taacttggca	ataaccagtc	ctggtgatac	ataaaactac	tcactgt	177

&lt;210&gt; 163

&lt;211&gt; 137

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(137)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 163

catttatata	gacaggcgtg	aagacattca	cgacaaaaac	gcgaaattct	atcccgtgac	60
canagaaggc	agctacggct	actcctacat	cctggcgtgg	gtggccttcg	cctgcacett	120
catcagcggc	atgatgt					137

&lt;210&gt; 164

&lt;211&gt; 469

&lt;212&gt; DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (469)

<223> n = A,T,C or G

<400> 164

cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta	60
tgcaatgcat catgctatct catacctaata gagggagttc caggagattc aaccaggaaa	120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt	180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg	240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg	300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct	360
tctagtaggc acagggtccc caggccaggc ctccattctcc tctggcctct aatagtcaat	420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt	469

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (195)

<223> n = A,T,C or G

<400> 165

acagtttttt atanatctg acattgcccg cacttggtgtt cagtttcata aagctgggtg	60
atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc	120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact	180
tcctctgaga tgagt	195

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (383)

<223> n = A,T,C or G

<400> 166

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc	60
cgaggtcgga gtccacacca ccggtgtagg tgtgtctaat cttgggcttg gcgcccacct	120
ttggagaagg gatatgtctg acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt	180
tttgacagacc agcctgagca aggggcggat gtccagcttc agctcctcct tcgtcagggtg	240
gatgccaaacc tcgtctangg tccgtgggaa gctgggtgtc acntcaccta caacctgggc	300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt	360
nggggccttt ttggtgaact ttc	383

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature  
 <222> (1)...(247)  
 <223> n = A,T,C or G

<400> 167  
 acagagccag accttgGCCa taaatgaanc agagattaag actaaacccc aagtcganat 60  
 tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120  
 tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180  
 tcaatctgan tccaaagtgg tggtcgaac actggtcatg acanaggcag tgactctgac 240  
 tgangtc 247

<210> 168  
 <211> 273  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(273)  
 <223> n = A,T,C or G

<400> 168  
 acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60  
 aatccctcan ccttgttctt caenactgtc tatactgana gtgtcatgtt tccacaaagg 120  
 gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtgggc 180  
 aattcccaac ttccttgcca caagcttccc aggttttctc ccctggaaaa ctccagcttg 240  
 agtcccagat acactcatgg gctgccttg gca 273

<210> 169  
 <211> 431  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(431)  
 <223> n = A,T,C or G

<400> 169  
 acagccttgG cttcccaaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60  
 agctcagacc aggggtcaaag gatgtgacat caacagtttc tggtttcaga acagggttcta 120  
 ctactgtcaa atgaccccc atacttcctc aaaggctgtg gtaagttttg cacagggtgag 180  
 ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240  
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc 300  
 acgcacatca ctgacaaccg ggatggaaaa agaantgcc aacttcatac atccaactgg 360  
 aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc 420  
 tcgaacactg a 431

<210> 170  
 <211> 266  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(266)  
 <223> n = A,T,C or G

&lt;400&gt; 170

```

acctgtgggc tgggctgtta tgctgtgcc ggctgtgaa agggagtcca gaggtggagc      60
tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact      120
ccccgctaga aagacaccag attggagtcc tgggaggggg agttggggtg ggcatttgat      180
gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct      240
tcaaagctag gggctctggca ggtgga                                     266

```

&lt;210&gt; 171

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1248)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 171

```

ggcagccaaa tcataaacgg cgaggactgc agccccgact cgcagccctg gcaggcggca      60
ctggctcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcacccgca gtgggtgctg      120
tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg      180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta      240
cggcaccag agtacaacag acccttgctc gctaaccgacc tcatgctcat caagttggac      300
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc      360
gcggggaaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc      420
gtgctgcagt gcgtgaacgt gtccgtgggtg tctgaggagg tctgcagtaa gctctatgac      480
ccgctgtacc accccagcat gttctgcgcc ggcggagggg aagaccagaa ggactcctgc      540
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtcttct      600
ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc      660
actgagtga tagaaaaac cgtccaggcc agttaactct ggggactggg aacctatgaa      720
attgacccc aaatacatcc tgcggaagga attcaggaa atctgttccc agcccctcct      780
ccctcaggcc caggagtcca ggccccagc ccctcctccc tcaaaccaag ggtacagatc      840
cccagcccct cctccctcag acccaggagt ccagaccccc cageccctcc tccctcagac      900
ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag cccctcctcc      960
ctcagacca ggggtccagg cccccaacct ctctcctcc agactcagag gtccaagccc      1020
ccaaccntc attccccaga cccagaggtc cagggtccag cccctcntcc ctcagacca      1080
gcggtccaat gccacctaga cnttcctgt acacagtgcc cccttggtgc acgttgacct      1140
aaccttacca gttggttttt ctttttngt ccctttcccc tagatccaga aataaagttt      1200
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1248

```

&lt;210&gt; 172

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(159)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 172

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1              5              10              15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
              20              25              30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
              35              40              45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly

```

50	55	60
Arg Met Pro Thr Val	Leu Gln Cys Val Asn Val Ser Val Val Ser Glu	
65	70	75
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe		80
	85	90
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser		95
	100	105
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe		110
	115	120
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn		125
	130	135
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		140
145	150	155

&lt;210&gt; 173

&lt;211&gt; 1265

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1265)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 173

ggcagcccg	actgcagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgttctgc	60
tcgggcgtcc	tggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggcct	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gacccttgct	cgctaacgac	240
ctcatgtctca	tcaagttgga	cgaatccgtg	tccgagtctg	acaccatccg	gagcatcagc	300
attgcttcgc	agtgccctac	cgcggggaac	tcttgctcgc	tttctggctg	gggtctgctg	360
gcgaacggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggtcctc	tgcccagtcg	420
cgggggctga	cccagagctc	tgcggtccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcggg	ggtgtctgag	gaggtctgca	gtaagctcta	tgaccgcgtg	taccacccca	540
gcatgttctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacggg	gactctgggg	600
ggccctgat	ctgcaacggg	tacttgagg	gccttggtgc	tttcggaaaa	gccccgtgtg	660
gccaaagtgg	cgtgccagg	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tggaacccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcctccctca	ggcccaggag	840
tccaggcccc	cagcccctcc	tccctcaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagacccag	gagtccagac	ccccagcccc	ctcctccctc	agaccagga	gtccagcccc	960
tcctccntca	gaccaggag	tccagacccc	ccagccctc	ctcctcaga	cccaggggtt	1020
gaggccccca	accctcctc	cttcagagtc	agagggtcaa	gcccccaacc	cctcggtccc	1080
cagacccaga	ggttnaggtc	ccagcccctc	ttccntcaga	cccagnngtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcccccttg	tggnangttg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

&lt;210&gt; 174

&lt;211&gt; 1459

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1459)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 174

ggtcagccgc	acactgtttc	cagaagtgcg	tgcagagctc	ctacaccatc	gggctggggc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagttag	180
acgaatccgt	gtccgagctc	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcctta	240
ccgcggggaa	ctcttgccct	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	accagagctc	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgacccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
cagggaaagg	tggagaagg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
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ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgagggcggg	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tggttgcaact	ctcctaaaa	ttttctgatg	tgtttattga	1020
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gtaccagag	ggaaacagtg	acacagatcc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aaatcaagac	tctacaaaga	ggctggggcag	ggtggctcat	gcctgtaate	ccagcacttt	1200
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aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagagggt	1380
gaagtgcgtt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

&lt;210&gt; 175

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1167)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 175

gcgcagccct	ggcaggcggc	actggtcagt	gaaaacgaat	tggtctgctc	gggcgtcctg	60
gtgcatccgc	agtggtgctc	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccaga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcctc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	300
tgccctaccg	cggggaaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcactg	cgtgaacgtg	tcgggtggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgcgg	gcggaggggca	agaccagaag	480
gactcctgca	acggtgactc	tgggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
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tgcaaatcca	ctgagtggat	agagaaaaacc	gtccagncca	gttaactctg	gggactggga	660
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gtacagatcc	ccagccctc	ctccctcaga	cccaggagtc	cagaccccc	agccctcnt	840
ccntcagacc	caggagtcca	gcccctcctc	cntcagacgc	aggagtccag	acccccagc	900
ccntcntccg	tcagaccag	gggtgcaggc	ccccaacccc	tcntcntca	gagtcagagg	960
tccaagcccc	caaccctc	ttccccagac	ccagaggtnc	aggtcccagc	ccctcctccc	1020
tcagaccag	cggccaatg	ccacctagan	tnccctgta	cacagtgcgc	ccttgtggca	1080
ngttgaccca	accttaccag	ttggttttct	attttttgct	cctttccct	agatccagaa	1140
ataaagtnta	agagaagcgc	aaaaaaa				1167

<210> 176  
 <211> 205  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(205)  
 <223> Xaa = Any Amino Acid

<400> 176  
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp  
 1 5 10 15  
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
 20 25 30  
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val  
 35 40 45  
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu  
 50 55 60  
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100 105 110  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115 120 125  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130 135 140  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145 150 155 160  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165 170 175  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180 185 190  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195 200 205

<210> 177  
 <211> 1119  
 <212> DNA  
 <213> Homo sapien

<400> 177  
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 gtcttggtgc atccgcagt ggtgctgtca gccgcacact gtttccagaa ctctacacc 120  
 atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag 180  
 gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg 240  
 ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct 300  
 tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctggggtct gctggcgaa 360  
 gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420  
 caacctggc agggttgtac catttcggca acttcagtg caaggacgtc ctgctgcatc 480  
 ctactgggt gctcactact gctcactgca tcaccggaa cactgtgatc aactagccag 540  
 caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600  
 actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660  
 cagttatcct cactgaattg agatttctctg cttcagtgtc agccattccc acataatttc 720  
 tgacctacag aggtgagga tcatatagct cttcaaggat gctggtactc ccctcacaaa 780

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ttcattttctc ctgttgtagt gaaagggtgcg ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg     1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc     1080
ttaataaaca gaagctgtga tgtaaaaaaa aaaaaaaaaa     1119

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&lt;210&gt; 178

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1) ... (164)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1              5              10              15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
              20              25              30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
              35              40              45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
              50              55              60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65              70              75              80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
              85              90              95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
              100             105             110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
              115             120             125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130             135             140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145             150             155             160
Pro Gly Thr Leu

```

&lt;210&gt; 179

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 179

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct      60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct     120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga     180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa     240
aaaaaaaaaa                                     250

```

&lt;210&gt; 180

&lt;211&gt; 202

&lt;212&gt; DNA

&lt;213&gt; Homo sapien



<400> 180  
 actagtccag tgtgggtggaa ttccattgtg ttggggcccaa cacaatggct acctttaaca 60  
 tcacccagac cccgccccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta 120  
 ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttggt tataaatgcc 180  
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181

<211> 558

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(558)

<223> n = A,T,C or G

<400> 181  
 tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg 60  
 aatgttttagg cagtgtcagt aatttcytcg taatgattct gttattactt tcctnattct 120  
 ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa 180  
 ggtagtgtga tagtataagt atctaagtc agatgaaagt gtgttatata tatccattca 240  
 aaattatgca agtttagtaat tactcaggt taactaaatt actttaatat gctgttgaac 300  
 ctactctgtt ccttggttag aaaaaattat aaacaggact ttgttagttt gggaagccaa 360  
 attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw 420  
 ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt 480  
 aaaaacagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc 540  
 caaaaaaaaa aaaaaaaaaa 558

<210> 182

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 182  
 acagggwttk grgatgcta agsccccrga rwtggtttga tccaacctg gcttwttttc 60  
 agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmg gcacccctgg 120  
 cstcacacag astcccagat agctgggact acaggcacac agtcactgaa gcaggccctg 180  
 ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca 240  
 ctaagggttaa actttcccac ccagaaaagg caacttagat aaaatccttag agtactttca 300  
 tactmttcta agtcctcttc cagcctcact kkgagtccm cytggggggt gataggaant 360  
 ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg gatagcatara 420  
 awtgstgata aaattaaaat gttctggtty mactttaaaa aaaaaaaaaa aaaaaaaaaa 479

<210> 183

<211> 384

<212> DNA

<213> Homo sapien

<400> 183  
 aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60  
 agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgtc 120  
 ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt 180  
 gccagcacca gtggcagctc tgggtgctgt ggtttctcct acaagtgaga ttttagatat 240

tgттаатсст gccagtcttt ctcttcaagc caggggtgcat cctcagaaac ctactcaaca	300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt	360
gccatttcaa aaaaaaaaaa aaaa	384

&lt;210&gt; 184

&lt;211&gt; 496

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(496)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 184

accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatkac ctcaacgagc	60
aggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgctcag	120
cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga	180
aacgcttcaa ggtgctcatg acccagcaac cgcgcctgt cctctgaggg tcccttaaac	240
tgatgtcttt tctgccacct gttacccctc ggagactccg taaccaaact cttcggactg	300
tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg	360
attatgcttg tgtgaggcaa tcatggtggc atcacccata aagggaacac atttgacttt	420
ttttctcat attttaaat actacmagaw tattwmagaw waaatgawtt gaaaaactst	480
taaaaaaaaa aaaaaa	496

&lt;210&gt; 185

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 185

gctggtagcc tatggcgkgg ccacggagg ggctcctgag gccacggrac agtgacttcc	60
caagtatcyt gcgscgctc ttctaccgtc cctacctgca gatcttcggg cagattcccc	120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcgag cccggcttct	180
gggcacaccc tcttggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg	240
tggtgctgct cctcgtcatc ttctgctcg tggccaacat cctgctggtc aacttgctca	300
ttgccatggt cagttacaca ttcggcaaaag tacagggcaa cagcgaatctc tactgggaag	360
gcgcagcggt accgcctcat ccgg	384

&lt;210&gt; 186

&lt;211&gt; 577

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(577)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 186

gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc	60
tnccatcgtc atactgtagg tttgccacca cytcctggca tcttggggcg gcntaatatt	120
ccaggaaact ctcaatcaag tcaccgtcga tgaaacctgt gggctgggtc tgtcttccgc	180
tcggtgtgaa aggatctccc agaaggagtg ctcgatcttc cccacacttt tgatgacttt	240
attgagtcga ttctgcatgt ccagcaggag gttgtaccag ctctctgaca gtgaggtcac	300
cagccctatc atgcccgtga mcgtgccgaa garcaccgag ccttgtgtgg gggkkgaggt	360
ctcaccacaga ttctgcatta ccagagagcc gtggcaaaag acattgacaa actcgcccag	420
gtggaaaaag amcamctcct ggargtgctn gccgctctc gtcmgttggt ggcagcgctw	480

tccttttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcacatcc 540  
 aagatntcgc acagcactna tccagttggg attaaat 577

<210> 187  
 <211> 534  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(534)  
 <223> n = A,T,C or G

<400> 187  
 aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgstg agaaticatw 60  
 actkggaaaa gmaacattaa agcctggaca ctggtattaa aattcacaat atgcaacact 120  
 ttaaacagtg tgtcaatctg ctcccyynac tttgtcatca ccagtctggg aakaagggtta 180  
 tgccttatcc acacctgtta aaagggcgct aagcattttt gattcaacat cttttttttt 240  
 gacacaagtc cgaaaaaagc aaaagttaaag agttatyaat ttgttagcca attcactttc 300  
 ttcattgggac agagccatyt gatttaaaaa gcaaattgca taatattgag ctttygggagc 360  
 tgatatttga gcggaagagt agcctttcta cttcaccaga cacaactccc tttcatattg 420  
 ggatgttnac naaagtwtatg tctctwacag atgggatgct tttgtggcaa ttctgttctg 480  
 aggatctccc agtttattta ccacttgcaac aagaaggcgt tttcttctc aggc 534

<210> 188  
 <211> 761  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(761)  
 <223> n = A,T,C or G

<400> 188  
 agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaatth tgtgtgcgtg 60  
 tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg 120  
 cctcttttgt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180  
 ttgtcttctg tgtaaatggg actagagaaa acacctatnt tatgagtcaa tctagttngt 240  
 tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg 300  
 ggggacaaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa 360  
 acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtkt wttctccctt 420  
 gcaaaaaaca tgtacngact tcccgttgag taatgccaag ttgttttttt tatnataaaa 480  
 cttgcccttc attacatggt tnaaagtggg gtgggtgggc aaaatattga aatgatggaa 540  
 ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac 600  
 atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta 660  
 tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac 720  
 gaaaataata acattgaaga aaaaananaa aaanaaaaaa a 761

<210> 189  
 <211> 482  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(482)  
 <223> n = A,T,C or G

```

<400> 189
tttttttttt tttgccgatn ctactatattt attgcaggan gtgggggtgt atgcaccgca      60
caccggggct atnagaagca agaaggaagg agggagggca cagcccttg ctgagcaaca      120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcc aggggtggga atacagggg tgggagtgt gcataagaag      240
tgataggcac aggccaccg gtacagacc ctcggtcct gacaggtnga ttctgaccag      300
gtcattgtgc cctgccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc      360
aaatttggtc ngtcatngaa ngggcanttt tccaantnng gctnngtctt ggtacncttg      420
gttcggccca gtcncnctc caaaaantat tcaccnctt ccnaattgct tgcngncccc      480
cc                                                                                   482

```

<210> 190

<211> 471

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(471)

<223> n = A,T,C or G

```

<400> 190
tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtntctca      120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c                    471

```

<210> 191

<211> 402

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(402)

<223> n = A,T,C or G

```

<400> 191
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct      60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa      120
attcttcacc agtcacatct tctaggacct ttttggtatc agttagtata agctcttcca      180
cttcctttgt taagacttca tctggtaaag tcttaagttt ttagaagg aattyaattg      240
ctcgttctct aacaatgtcc tctccttgaa gtatttggtc gaacaaccca cctaaagtcc      300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc      360
aagagtcatc tgtctgcaaa agttgcgtta gtatatctgc ca                    402

```

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

&lt;222&gt; (1)...(601)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 192

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcytyttt	gaytaccgtg	tgccaagtgc	tgggtgattct	yaacacacyt	ccatcccgyt	180
cttttgtgga	aaaactggca	cttkctctgga	actagcarga	catcacttac	aaattcaccc	240
acgagacact	tgaaagggtg	aacaaagcga	ytcttgcat	gctttttgtc	cctccggcac	300
cagttgtcaa	tactaaccgg	ctgggttgcc	tccatcacat	ttgtgatctg	tagctctgga	360
tacatctcct	gacagtactg	aagaacttct	tcttttgttt	caaaagcarg	tcttgggtgcc	420
tgttggatca	ggttccccatt	tcccagtcyg	aatgttcaca	tggcatat	wacttcccac	480
aaaacattgc	gatttgaggc	tcagcaacag	caaatcctgt	tccggcattg	gctgcaagag	540
cctcgatgta	gccggccagc	gccaaggcag	gcgccgtgag	ccccaccagc	agcagaagca	600
g						601

&lt;210&gt; 193

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(608)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 193

atacagccca	natcccacca	cgaagatgcg	cttggtgact	gagaacctga	tgcggtcact	60
ggtcccgtcg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgcaactcytt	120
cccaacgcag	gcagmagcgg	gsccgggtcaa	tgaactccay	tcgtggcttg	gggtkgacgg	180
tkaagtgcag	gaagaggctg	accacctcgc	ggtccaccag	gatgcccagc	tgtgcgggac	240
ctgcagcgaa	actcctcgat	ggtcatgagc	gggaagcgaa	tgaggcccag	ggccttgccc	300
agaaccttcc	gcctgttctc	tggcgtcacc	tgcaagctgt	gccgctgaca	ctcgggcctcg	360
gaccagcgga	caaacggcrt	tgaacagccg	cacctcacgg	atgcccagtg	tgctcgcgctc	420
caggammgsc	accagcgtgt	ccagggtcaat	gtcgggtgaag	ccctccgcgg	gtrattggcgt	480
ctgcagtgtt	tttgcgatg	ttctccaggc	acaggctggc	cagctgcggg	tcacgaaga	540
gtcgcgcctg	cgtgagcagc	atgaaggcgt	tgctcggtcg	cagttcttct	tcaggaactc	600
cacgcaat						608

&lt;210&gt; 194

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(392)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 194

gaacggctgg	accttgccctc	gcattgtgct	tgctggcagg	gaataccttg	gcaagcagyt	60
ccagtcogag	cagccccaga	ccgctgccgc	ccgaagctaa	gcctgcctct	ggccttcccc	120
tccgcctcaa	tgacgaacca	gtagtgggag	cactgtgttt	agagttaaga	gtgaacactg	180
tttgatttta	cttgggaatt	tctctgttta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgctgttt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtattttatt	gktinctstgg	360
aaataaatat	agttattaaa	ggttgtcant	cc			392

<210> 195  
 <211> 502  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(502)  
 <223> n = A,T,C or G

<400> 195  
 ccsttkgagg ggkagggkyc cagtttccga gtggaagaaa caggccagga gaagtgcgtg 60  
 ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc 120  
 cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc 180  
 aagggaaggc cccattccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc 240  
 ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca 300  
 caaatgcaag ctcaccaagg tccccctcga gtccccctcc stacaccctg amcggccact 360  
 gscscacacc caccagagc acgccacccg ccatggggar tgtgctcaag gartcgcnng 420  
 gcacgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt 480  
 gctnanaaaa aaaaanaaaa aa 502

<210> 196  
 <211> 665  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(665)  
 <223> n = A,T,C or G

<400> 196  
 gggtacttgg ttctattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60  
 cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt 120  
 wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawtga 180  
 actwatattat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkatc 240  
 aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300  
 attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatataatgcc ttttgtaact 360  
 tcacttgggtt attttattgt aaatgartta caaaattctt aatttaagar aatggtatgt 420  
 watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcattgatt 480  
 tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt 540  
 ttcttagaat gtataaagggt ttagagccat cnaacttcaa agaaaaaat gaccacatac 600  
 tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660  
 aagtg 665

<210> 197  
 <211> 492  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(492)  
 <223> n = A,T,C or G

<400> 197  
 tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat 60  
 atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120

```

aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag      180
aattatagtc naaccagtaa acnaggaatt tactttttcaa aagattaaat ccaaactgaa      240
caaaatttcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgatac      300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct      360
tgttcaaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc      420
catttcactc ccatacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg      480
ancntggctt aa                                                              492

```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

```

ttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa      60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac      120
tgagtatat ttgaaaaagg caagttttaa gtanacncat attgccganc atancacatt      180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat      240
natatatgtc aatcngatth aagatacaaa acagatccta tggtagatan catcntgtag      300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta      360
agcattctag tacctctact ccatggttaa gaatcgtaca cttatgttta catatgtnc      420
gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa      478

```

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 199

```

agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta      60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca      120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga      180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatattctca tgcagcttta      240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga      300
aaatttacct ggangaaaag aggcttngg ctggggacca tccattgaa cttctcttta      360
anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg      420
aacntngacn ncacccttnt ggaatanant cttgacngcn tctgaactt gtcctctgc      480
ga

```

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(270)

<223> n = A,T,C or G

<400> 200						
cggccgcaag	tgcaactcca	gctggggccg	tgcggacgaa	gattctgcc	gcagttggtc	60
cgactgcgac	gacggcggcg	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgcgcga	gaggtcgtgt	cacgtcccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggt	gaangcggga	ggcctcgggg	agccctcg	gaagggcggc	240
ccgagagata	cgcaggtgca	ggtggccgcc				270

```
<210> 201
<211> 419
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(419)
<223> n = A,T,C or G
```

<400> 201						
tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttatttttgca	60
gctagcaagg	taacagggta	gggcatgggt	acatgttcag	gtcaacttcc	tttgctcgtgg	120
ttgattgggt	tgtcttttatg	ggggcggggg	ggggtagggg	aaancgaagc	anaantaaca	180
tggagtgggt	gcacctctcc	tgtagaacct	ggttacnaaa	gcttgggggc	gttcacctgg	240
tcctgtgacc	tcattttctt	gacatcaatg	ttattaggaag	tcaggatatc	ttttagagag	300
tccactgtnt	ctggagggag	attaggggtt	cttgcgaana	tccaancaaa	atccacntga	360
aaaagttgga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cgggtggcca	419

```
<210> 202
<211> 509
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1) ... (509)
<223> n = A,T,C or G
```

<400> 202							
tttntttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt		60
tggcacttaa	tccattttta	tttcaaaatg	tctacaaant	ttnaatncnc	cattatacng		120
gtnattttnc	aaaatctaaa	nnttatctaa	atntnagcca	aantccttac	ncaaatnnaa		180
tacnncaaaa	aatcaaaaat	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa		240
aatatatacg	gctgggtgtt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnnaa		300
ggaactaaaa	taaaaaaaaa	cactnccgca	aagggtaaag	ggaacaacaa	attcntttta		360
caacancnnc	nattataaaa	atcatatctc	aaatcttagg	ggaatatata	cttcacacng		420
ggatctttaac	ttttactnca	ctttgtttat	ttttttanaa	ccattgnttt	gggcccacaa		480
caatggnaat	nccnccnnc	tggactagt					509

```
<210> 203
<211> 583
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1) ... (583)
<223> n = A,T,C or G
```



&lt;400&gt; 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaag	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tcctatttcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tattttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggcttaga	tccttttatg	480
tccatttttag	tcactaaacg	atatacnaag	tgccagaatg	caaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

&lt;210&gt; 204

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(589)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 204

ttttttttnt	tttttttttt	tttttttctc	ttcttttttt	ttganaatga	ggatcgagtt	60
tttactcttc	tagatagggc	atgaagaaaa	ctcatctttc	cagcttttaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagagggtt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttggtta	gnntatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

&lt;210&gt; 205

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(545)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 205

tttttntttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacat	agtaaatat	180
ttaagatcat	agagcttgta	agtgaagaaa	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggacttctt	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaaac	caacacattc	tgaaggatac	attacttagt	gatagattct	360
tatgtacttt	gctanattac	gtggatatga	gttgacaaag	ttctctttct	tcaatctttt	420
aagggggcnga	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480
aaggattaga	tatgttttct	ttgccaatat	taaaaaaaata	ataatgttta	ctactagtga	540
aaccc						545

&lt;210&gt; 206

&lt;211&gt; 487

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

tttttttttt	tttttttagtc	aagtttctna	tttttattat	aattaaagtc	ttggtcattt	60
catttatttag	ctctgcaact	tacatattta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggtg	ccattattga	gtanatatat	tcctccaaga	gtggatgtgt	180
cccttctccc	accaactaat	gaancagcaa	cattagtttta	attttattag	tagatnatac	240
actgctgcaa	acgctaattc	tcttctccat	ccccatgtng	atattgtgta	tatgtgtgag	300
ttggtnagaa	tgcatacanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcggtgaaaa	tagactgtgt	ctgtctgaat	caaatgatct	gacctatcct	cgggtggcaag	420
aactcttcga	accgcttctc	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480
ttcaaaa						487

<210> 207

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 207

tgaattggct	aaaagactgc	atttttanaa	ctagcaactc	ttatttcttt	cctttaaaaa	60
tacatagcat	taaatcccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atctttgcat	gcagaggagg	taaaagggtat	tggattttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaaagaaggc	agcctaggcc	ctggggagcc	ca			332

<210> 208

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 208

agggcggtgt	gcggagggcg	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttgtgttcc	ggccccatcc	aaccacgaag	ttgattttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtgtaagg	gcacactcac	180
tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcgaaa	tacttnttga	aacttgcaga	tgataactaa	gatccaagat	atttcccaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgatcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

<210> 209  
 <211> 159  
 <212> DNA  
 <213> Homo sapien

<400> 209  
 ggggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg 60  
 tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca 120  
 caaaggactc tcgacccaaa ctgccccaga ccctctcca 159

<210> 210  
 <211> 256  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(256)  
 <223> n = A,T,C or G

<400> 210  
 actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc 60  
 actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120  
 tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180  
 ttgcagggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240  
 ccaggatgct aatatca 256

<210> 211  
 <211> 264  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(264)  
 <223> n = A,T,C or G

<400> 211  
 acattgtttt tttagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga 180  
 ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240  
 aaaaaaggag caaatgagaa gcct 264

<210> 212  
 <211> 328  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(328)  
 <223> n = A,T,C or G

<400> 212  
 acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60  
 ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120  
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180

ttnaatttca ttccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta	240
cccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca	300
tttttttttc ctttattcct ttgtcaga	328

&lt;210&gt; 213

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (250)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 213

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggt	250

&lt;210&gt; 214

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (444)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 214

accagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag	60
gatttaagt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc gacaacaggc tattgaactt gcccgccagt	180
tgaatttcat tcccattgac ttgggaccc tatcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc cagtgggtgg agctataagc ttggccacat	300
tttttttttc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag	360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc	444

&lt;210&gt; 215

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (366)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 215

acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct	240
tctcatcggt aagcagagggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa	300
tccaagctgt tttctacact gtaaccagggt ttccaaccaa ggtggaaatc tcctatactt	360

ggtgcc

366

<210> 216  
 <211> 260  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(260)  
 <223> n = A,T,C or G

<400> 216  
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60  
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120  
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180  
 atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240  
 aattcttctt tccctccttt 260

<210> 217  
 <211> 262  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(262)  
 <223> n = A,T,C or G

<400> 217  
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60  
 tcttgcttat aattttctat tttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120  
 ggattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180  
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240  
 atatccttca tgcttgtaaa gt 262

<210> 218  
 <211> 205  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(205)  
 <223> n = A,T,C or G

<400> 218  
 accaaggtgg tgcattaccg gaantggatc aangacacca tctgggcaa cccctgagca 60  
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120  
 aggcctcccc agttctactg acctttgtcc ttangntntna ngtcagggt tgctaggaaa 180  
 anaaatcagc agacacagggt gtaaa 205

<210> 219  
 <211> 114  
 <212> DNA  
 <213> Homo sapien

<400> 219

tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60  
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220  
<211> 93  
<212> DNA  
<213> Homo sapien

<400> 220  
actagccagc acaaaaaggca gggtagcctg aattgctttc tgetctttac atttttttta 60  
aaataagcat ttagtgctca gtcctactg agt 93

<210> 221  
<211> 167  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(167)  
<223> n = A,T,C or G

<400> 221  
actangtgca ggtgcgcaca aatatttgtc gatattccct tcatcttggga ttccatgagg 60  
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120  
ccccactac cttccctgac gtcceccana aatcacccaa cctctgt 167

<210> 222  
<211> 351  
<212> DNA  
<213> Homo sapien

<400> 222  
agggcgtggt gcggagggcg gtactgacct cattagtagg aggatgcatt ctggcacccc 60  
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa 120  
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180  
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240  
taggtgagca tgattagaga gctttaggt tgcttttaca tatatctggc atatttgagt 300  
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t 351

<210> 223  
<211> 383  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(383)  
<223> n = A,T,C or G

<400> 223  
aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60  
tggtaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga 120  
ttaaagtgtc tgtgccaaaa ttttgtatth tatttgagga cttcttatca aaagtaatgc 180  
tgccaaagga agtctaagga attagtagtg ttcccmteac ttgtttggag tgtgctatc 240  
taaaagatth tgatttcctg gaatgacaat tatattttta ctttggtggg ggaaanagtt 300  
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg 360  
accattaagc tatatgttta aaa 383

<210> 224  
 <211> 320  
 <212> DNA  
 <213> Homo sapien

<400> 224  
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60  
 aaaagtttgt gacattgttag tagggagtgt gtacccttta ctccccatca aaaaaaaaaat 120  
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180  
 gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac 240  
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgacgt 300  
 tttaractcm gcattgtgac 320

<210> 225  
 <211> 1214  
 <212> DNA  
 <213> Homo sapien

<400> 225  
 gaggactgca gcccgcactc gcagccctgg caggcggcac tggtcattgga aaacgaattg 60  
 ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag 120  
 aactcctaca ccatacgggt gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180  
 cagatgggtgg aggccagcct ctccgtacgg caccagagt acaacagacc cttgctcgtc 240  
 aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300  
 atcagcattg cttcgcagtg ccctaccgcg gggaactctt gcctcgtttc tggctgggggt 360  
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtgggtgtc 420  
 gaggaggtct gcagtaagct ctatgaccgg ctgtaccacc ccagcatgtt ctgcgcgcggc 480  
 ggagggcaag accagaagga ctctgcaac ggtgactctg gggggcccct gatctgcaac 540  
 gggtaacttg agggccttgt gtctttcgga aaagcccggt gtggccaagt tggcgtgcc 600  
 ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660  
 taactctggg gactgggaac ccatgaaatt gacccccaaa tacatcctgc ggaaggaatt 720  
 caggaatata tgttcccagc ccctcctccc tcaggcccag gagtccaggc cccagcccc 780  
 tcctccctca aaccaagggt acagatcccc agccccctct ccctcagacc caggagtcca 840  
 gacccccag cccctcctcc ctccagacca ggagtccagc ccctcctccc tcagaccag 900  
 gagtccagac cccccagccc ctctcctc agaccaggg gtccaggccc ccaaccctc 960  
 ctccctcaga ctccagggc caagcccca accctcctt cccagaccc agaggtccag 1020  
 gtcccagccc ctctcctc agaccagcg gtccaatgcc acctagactc tccctgtaca 1080  
 cagtgcctcc ttgtggcagc ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140  
 tttccctag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaaaaaaaa aaaa 1214

<210> 226  
 <211> 119  
 <212> DNA  
 <213> Homo sapien

<400> 226  
 acccagtatg tgcagggaga cggaaccca tgtgacagcc cactccacca gggttcccaa 60  
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<400> 227  
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acggacggtt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aaggtggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
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gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagt ttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

&lt;210&gt; 228

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaacga	gcctcctcct	tggaagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
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tgctcgggtc	acattggggg	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtcc	acctctgcag	360
gctggcagct	gaatggcttg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggttgg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgaaccg	540
ccgtgggtatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggttg	600
ttcttttctg	taatgttctc	ctgtgttgct	agctgtcttc	atttcctggg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttccactctg	aagtagctgg	tggt				744

&lt;210&gt; 229

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcatgtgaac	60
cattacacat	cgaaataaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacagct	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagtct	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

&lt;210&gt; 230

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 230

cagcagaaca	aatacaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120
caatataaag	tcctgggttc	cactcaggaa	cgagagctga	cccagtttaag	ggagaagttg	180
cggaaggga	gagatgcctc	cctctcattg	aatgagcatc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	ccgcgaccac	300
g						301



<210> 231  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 231  
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 caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120  
 ggcaacacgg gactttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180  
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtta ccgccaatga tgaacacatt 240  
 tttttttgtg gacatgccat ccattttctgt caggatctgg ttgatgactc ggtcagcagc 300  
 c 301

<210> 232  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 232  
 agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagtctctcc ttcaagtgtt 60  
 ggcgacagcg gggcttcctg attctggaat ataactttgt gttaaattaac agccacctat 120  
 agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtccctgtcca 180  
 cgtgctgtac caagtgtctg tgccagcctg ttacctgttc tcaactgaaaa tctggctaata 240  
 gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300  
 g 301

<210> 233  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 233  
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 cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc 180  
 gagttagctg gactacaggg acacagtcac tgaagcaggc cctgttagca attctatgag 240  
 taaaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300  
 c 301

<210> 234  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 234  
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 cattttatcc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt 120  
 tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180  
 cgcctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240  
 ttgatcacca gcttaatggg cagatcatct gttcaatgg cttcgtcagt atagttcttc 300  
 t 301

<210> 235  
 <211> 283  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 235

tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg	60
aattccctca tcttttaggg aatcatttac caggtttggg gaggattcag acagctcagg	120
tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata	180
atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca	240
ttagggattc aaagaaatat tagatttaag ctcacactgg tca	283

&lt;210&gt; 236

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 236

aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata	60
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg	120
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatag	180
tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta	240
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc	300
a	301

&lt;210&gt; 237

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 237

cagtggtagt ggtggtggac gtggcggttg tcgtggtgcc ttttttggtg cccgtcacaa	60
actcaatttt tggtcgtccc tttttggcct tttccaattt gtccatctca attttctggg	120
ccttggctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatacct	180
ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatacta	240
gggttccgaa attcttttct cctttggata atgtagttca tatccattcc ctcttttacc	300
t	301

&lt;210&gt; 238

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 238

gggcagggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt	60
gttcacagtt cagccccctg ctcaaaaaac caacgggcca gctaaggaga ggaggaggca	120
ccttgagact tccggagtcg aggcctctcca gggttcccca gcccatcaat cattttctgc	180
acccccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240
gtgtgggacc cagggctctgt tcttcacagt aggaggtgga agggatgact aatttcttta	300
t	301

&lt;210&gt; 239

&lt;211&gt; 239

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 239

ataagcagct aggggaattct ttatttagta atgtcctaac ataaaaagttc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgccg gcatacacag tatacaggtc cttcaggga	239

&lt;210&gt; 240

<211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 240  
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 gggatctgcc ctccagtggg acctttttaag gaagaagtgg gcccaagcta agttccacat 120  
 gctgggtgag ccagatgact tctgttcctt gggtcactttc ttcaatgggg cgaatggggg 180  
 ctgccagggt tttaaaatca tgcttcattt tgaagcacac gggtcacttca cctcctcac 240  
 gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc 300

<210> 241  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 241  
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 cctcttttga ggaaactcca gcagctatgt tgggtgtctt gagggaaatgc aacaaggctg 120  
 ctctccatg tattggaaaa ctgcaaaactg gactcaactg gaaggaagtg ctgctgccag 180  
 tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct 240  
 tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga 300  
 g 301

<210> 242  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 242  
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 tgtggcattt cctcattttc tacattgtag aatcaagagt gtaataaat gtatatcgat 120  
 gtcttcaaga atatatcatt cttttttcac tagaaccat tcaaaatata agtcaagaat 180  
 cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta 240  
 taagtacca aagttttata aatcaaaaagc cctaatagata accattttta gaattcaatc 300  
 a 301

<210> 243  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 243  
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 ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg 120  
 tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggtatga tgaccagcgt 180  
 gctggtttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtaaccog 240  
 tcactaccgc atgttcaga aaggacagga gacgtccacc aatcccattg cttccatttt 300  
 t 301

<210> 244  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 244  
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 gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120

ccagggacct	tgaaaacagt	tgacactgta	aggtgcttgc	tccccaagac	acatcctaaa	180
aggtgttgta	atgggtgaaaa	cgtcttcctt	ctttattgcc	ccttcttatt	tatgtgaaca	240
actgtttgtc	ttttgtgtat	cttttttaaa	ctgtaaagtt	caattgtgaa	aatgaatatc	300

&lt;210&gt; 245

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 245

gtctgagtat	ttaaaaatggt	attgaaatta	tccccaacca	atgttagaaa	agaaagaggt	60
tatatactta	gataaaaaat	gaggtgaatt	actatccatt	gaaatcatgc	tcttagaatt	120
aaggccagga	gatattgtca	ttaatgtara	cttcaggaca	ctagagtata	gcagccctat	180
gttttcaaag	agcagagatg	caattaaata	ttgttttagca	tcaaaaaggc	caactcaatac	240
agctaataaa	atgaaagacc	taatttctaa	agcaattctt	tataatttac	aaagttttaa	300
g						301

&lt;210&gt; 246

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 246

ggtctgtcct	acaatgcctg	cttcttgaaa	gaagtcggca	ctttctagaa	tagctaaata	60
acctgggctt	attttaaaga	actatttgta	gctcagattg	gttttcttat	ggctaaaata	120
agtgttctt	gtgaaaatta	aataaaacag	ttaattcaaa	gccttgatat	atgttaccac	180
taacaatcat	actaaatata	ttttgaagta	caaagtttga	catgctctaa	agtgacaacc	240
caaatgtgtc	ttacaaaaca	cgttcctaac	aaggtatgct	ttacactacc	aatgcagaaa	300
c						301

&lt;210&gt; 247

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 247

aggtcctttg	gcagggctca	tggatcagag	ctcaaactgg	agggaaaggc	atttcgggta	60
gcctaagagg	gcgactggcg	gcagcacaac	caaggaaaggc	aaggttgttt	ccccacgct	120
gtgtcctgtg	ttcagggtgcg	acacacaatc	ctcatgggaa	caggatcacc	catgcgctgc	180
ccttgatgat	caagggtggg	gcttaagtgg	attaagggag	gcaagttctg	ggttccttgc	240
cttttcaaac	catgaagtca	ggctctgtat	ccctcctttt	cctaactgat	attctaacta	300
a						301

&lt;210&gt; 248

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 248

aggtccttgg	agatgccatt	tcagccgaag	gactcttctw	ttcggaagta	caccctcact	60
attaggaaga	ttcttagggg	taatttttct	gaggaaggag	aactagccaa	cttaagaatt	120
acaggaagaa	agtggtttgg	aagacagcca	aagaaataaa	agcagattaa	attgtatcag	180
gtacattcca	gcctgttggc	aactccataa	aaacatttca	gattttaatc	ccgaatttag	240
ctaatagagac	tggatttttg	ttttttatgt	tgtgtgtcgc	agagctaaaa	actcagttcc	300
c						301

&lt;210&gt; 249

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 249

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gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcacttggag      60
ccctgacgct gctgtttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc      120
ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc      180
catcgtaatg aattatTTTTG aaaattaatt ccaccatcct ttcagattct ggatggaaaag      240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt      300
a                                                                                   301

```

&lt;210&gt; 250

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 250

```

ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacactttctc      60
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc      120
cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac      180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta      240
caataaaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc      300
a                                                                                   301

```

&lt;210&gt; 251

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 251

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gccgaggtcc tacatttggc ccagtttccc cctgcatcct ctccagggcc cctgcctcat      60
agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat      120
ggcagggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct      180
cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga      240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatattct      300
c                                                                                   301

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&lt;210&gt; 252

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 252

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gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata      120
tcatttcttt ttacttagga acccattcaa aatataagtc aagaatctta atatcaacaa      180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt      240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc      300
a                                                                                   301

```

&lt;210&gt; 253

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 253

```

ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctega ttctcgtacc      60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctccttagct      120

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tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg      180
gatttttttt cttagagaac caaaaaacat aaaaggagca agtcggactg aatacctgtt      240
tccatagtgc ccacagggtg ttctcacat tttctccata ggaaaatgct ttttcccaag      300
g                                                                 301

```

&lt;210&gt; 254

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 254

```

cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg      60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc      120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa      180
gaaaaaaata aagcttttga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc      240
acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc      300
t                                                                 301

```

&lt;210&gt; 255

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 255

```

agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa      60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagt tgaacttgat      120
tggtgatttt ttgagtctct caagcatctc ctaataccct caagggcctg agtagggggg      180
aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta      240
aacattatta aaaaacaaga acaaaacaaa aaaatagaga aaaaaaccac cccaacacac      300
aa                                                                 302

```

&lt;210&gt; 256

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 256

```

gttccagaaa acattgaagg tggcttccca aagtctaaact agggataccc cctctagcct      60
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc      120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat      180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt      240
gtggcctctc ggctgggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt      300
t                                                                 301

```

&lt;210&gt; 257

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 257

```

gttgtggagg aactctggct tgctcattaa gtcctactga ttttactat cccctgaatt      60
tccccactta tttttgtctt tcaactatcg aggccttaga agaggtctac ctgcctccag      120
tcttacctag tccagtctac ccctggagt tagaatggcc atcctgaagt gaaaagtaat      180

```

gtcacattac tcccttcagt gatttcttgt agaagtgcc aatccctgaat gccaccaaga 240  
 tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300  
 c 301

<210> 258

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 258

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 aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120  
 cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat ctttaactg 180  
 atgtctcggt cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240  
 tgggtgatccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac 300  
 t 301

<210> 259

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 259

tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60  
 gtgtcctgaa gtgatttggg cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120  
 gcaaagccat aagggaagccc aggattcctt gtgatcagga agtgggcccag gaaggctctgt 180  
 tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt 240  
 cccctccatc ttctcaagca gtgtccttgt tgagccattt gcateccttg ctccagggtg 300  
 c 301

<210> 260

<211> 301

<212> DNA

<213> Homo sapien

<400> 260

ttttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt 60  
 aagggtgtctt aacttgaaaa agattaggag tcaactgggtt acaagttata attgaatgaa 120  
 agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac 180  
 tagggcaaaa taaataagtg tgtggaagcc ctgataagtg ctttaataaac agactgattc 240  
 actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300  
 c 301

<210> 261

<211> 301

<212> DNA

<213> Homo sapien

&lt;400&gt; 261

```

aaatattcga gcaaatecctg taactaatgt gtctccataa aaggctttga actcagtga      60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt      120
agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aagggttcaat      180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag      240
ggcatgatga tcatccaaag cccagtgggc atttactcca gactttctgc aatgaagatc      300
a                                                                                   301

```

&lt;210&gt; 262

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 262

```

gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatec ctgagtcacc      120
cctagacttc ctaaaccaga tctctcgggg ctggaacctg gcaactctgc tttgtaatga      180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcce      240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat      300
c                                                                                   301

```

&lt;210&gt; 263

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 263

```

tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg      60
aaaattacta cttaatccta attcacaata acaatggcat taagggttga cttgagttgg      120
ttcttagtat tatttatggg aaataggtct ttaccacttg caaataactg gccacatcat      180
taatgactga cttcccagta aggctctcta aggggtaagt angaggatcc acaggatttg      240
agatgctaag gcccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg      300
g                                                                                   301

```

&lt;210&gt; 264

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 264

```

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc      60
aatgaatgac tctaaaaaca atatttacat ttaatggttt gtagacaata aaaaaacaag      120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag      180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac      240
acccttcata taaattcact atcttggtt gaggcactcc ataaaatgta tcacgtgcat      300
a                                                                                   301

```

&lt;210&gt; 265

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 265



```

tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcatctttgt      60
cttcttgga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta      120
catattcttg gaagtctcta atcaactttt gtccatttg tttcatttct tcaggaggga      180
ttttcagttt gtcaacatgt tctctaaca cacttgccca tttctgtaaa gaatccaaag      240
cagtcacaag ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg      300
c

```

```

<210> 266
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 266
taccgtctgc ctttctctcc atccaggcca tctgcgaatc tacatgggtc ctctatttcg      60
acaccagatc actctttcct ctaccacag gcttgctatg agcaagagac acaacctcct      120
ctcttctgtg ttccagcttc ttttctgtt cttccacccc cttaagttct attcctgggg      180
atagagacac caatacccat aacctctctc ctaagcctcc ttataacca ggggtgcacag      240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg      300
a

```

```

<210> 267
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 267
aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg      60
gttctcagtg ctgagtccat ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc      120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaagc      180
ctcattctga ttctctcct tcttttctt caagttggct ttctcacat cctctgttc      240
aattcgcttc agcttgctg ctttagccct catttccaga agcttcttct ctttggcatc      300
t

```

```

<210> 268
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 268
aatgtctcac tcaactactt ccagcctac cgtggcctaa ttctgggagt tttcttctta      60
gatcttgga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc      120
tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgtttagac tcttgggaata      180
tgctgggtgg ctcagtgagc ctttttgag aaagcaagta ttattcttaa ggagtaacca      240
cttccatttg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact      300
a

```

```

<210> 269
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 269
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat      60
aaaattacct ttattcacac atctcaaac aattctgcaa attcttagtg aagtttaact      120
atagtcacag accttaata ttcacattgt tttctatgtc tactgaaaat aagttcacta      180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca ccccaatta      240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc      300
t

```

<210> 270  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 270  
 cattgaagag cttttgCGAA acatcagaac acaagtGctt ataaaattaa ttaagcctta 60  
 cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120  
 gagcttgctg gtgcagtGca tattggataa cactattcat ggccgaattg atcaagtcaa 180  
 ccaactcctt gaactggatc atcagaagaa gggTggTgca cgatatactg cactagataa 240  
 tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300  
 a 301

<210> 271  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 271  
 aaaaggTtct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt 60  
 tttatagctc atcttttaggg ttgatattca gttcatGctt cccttgctgt tcttgatcca 120  
 gaattgcaat cacttcatca gctgtattc gtcccaattc tctataaagt gggTccaagg 180  
 tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt 240  
 tctctcctcc agatganaac tgatcatgCG cccacatttt gggTtttata gaagcagtca 300  
 c 301

<210> 272  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 272  
 taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaattgc 60  
 ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120  
 tccaataatt ccctcatgat gagcaagaaa aattctttgc gcaccctcc tgcattccaca 180  
 gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc 240  
 ctaaggactt ccattgcac tctacaata ttttctctac gcaccactag aattaagcag 300  
 g 301

<210> 273  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 273  
 acatgtgtgt atgtgtatct ttgggaaaaa aanaagacat cttgtttayt atttttttgg 60  
 agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa 120

```

gaaccgtcta aaaataaaat ttaccatgtc dtatatctct tatagtatgc ttatttcacc 180
tlytttctgt ccagagagag tatcagtgac ananatttma gggatgaamac atgmattggg 240
gggacttnty ttacngagm accctgcccg sgcgcctcg makengantt ccgcsananc 300
t 301

```

<210> 274

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 274

```

cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg 60
aacagtaaatt gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca 180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc 240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaagtc 300
c 301

```

<210> 275

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 275

```

tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
gggtgaaatt ggccaacttt ctattaactt atgttggaac ttttgccacc aacagtaagc 120
tgcccttct aataaaaagaa aattgaaagg tttctcacta aacggaatta agtagtgag 180
tcaagagact ccagggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat 300
a 301

```

<210> 276

<211> 301

<212> DNA

<213> Homo sapien

<400> 276

```

tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240
aaaactattc agtatgtttc cttgtcttca tgtctgagaa ggctctcctt caatggggat 300
g 301

```

<210> 277

<211> 301

<212> DNA

<213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 277  
 tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60  
 atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120  
 gaatcatggc actcctgata ctttcccaa tcaacactct caatgcccc cctcgtcct 180  
 caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240  
 gttcncgtgc gattacatct gaccagtctc ctttttccga agtcntccg ttcaatcttg 300  
 c 301

<210> 278  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 278  
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60  
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgatca 120  
 cagtctctac tgttattatg cattacctgg gaatttataat aagcccttaa taataatgca 180  
 aatgaacatc tcatgtgtgc tcacaatggt ctggcactat tataagtgtc tcacaggttt 240  
 tatgtgttct tcgtaacttt atggantagg tactcgccg cgaacacgct aagccgaatt 300  
 c 301

<210> 279  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 279  
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60  
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120  
 ttagaccttt acctccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180  
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240  
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300  
 a 301

<210> 280  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 280  
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60  
 tagaaaggtg gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120

tgagaaaaaa	acctaagatt	agcccaggta	gttgccctgta	acttcagttt	ttctgcctgg	180
gtttgatata	gttttagggt	gggggttagat	taagatctaa	attacatcag	gacaaagaga	240
cagactatta	actccacagt	taattaagga	ggatatgtcc	atgtttat	gttaaagcag	300
t						301

&lt;210&gt; 281

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 281

aggtacaaga	aggggaatgg	gaaagagctg	ctgctgtggc	attgttcaac	ttggatat	60
gccgagcaat	ccaaatcctg	aatgaagggg	catcttctga	aaaaggagat	ctgaatctca	120
atgtggtagc	aatggcctta	tcgggttata	cggatgagaa	gaactccctt	tggagagaaa	180
tgtgtagcac	actgcgatta	cagctaaata	acccgtat	gtgtgtcatg	tttgcatttc	240
tgacaagtga	aacaggatct	tacgatggag	ttttgtatga	aaacaaagtt	gcagtacctc	300
g						301

&lt;210&gt; 282

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 282

caggtagtac	agaattaaaa	tactgacaag	caagtagttt	cttggcgtgc	acgaattgca	60
tccagaaccc	aaaaattaag	aaattcaaaa	agacattttg	tgggcacctg	ctagcacaga	120
agcgagaag	caaagcccag	gcagaacat	gctaacctta	cagctcagcc	tgcacagaag	180
cgagaagca	aagcccaggc	agaacatgc	taaccttaca	gctcagcctg	cacagaagcg	240
cagaagcaaa	gcccaggcag	aacatgctaa	ccttacagct	cagcctgcac	agaagcacag	300
a						301

&lt;210&gt; 283

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 283

atctgtatac	ggcagacaaa	ctttatarag	tgtagagagg	tgagcgaaag	gatgcaaaag	60
cactttgagg	gctttataat	aatatgctgc	ttgaaaaaaa	aaatgtgtag	ttgatactca	120
gtgcatctcc	agacatagta	aggggttgct	ctgaccaatc	aggatgatcat	tttttctatc	180
acttcccagg	ttttatgcaa	aaattttgtt	aaattctata	atggatgat	gcattcttta	240
ggaaacatat	acatttttta	aaatctat	tatgtaagaa	ctgacagacg	aatttgcttt	300
g						301

&lt;210&gt; 284

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 284

caggtagcaaa	acgctattaa	gtggcttaga	atttgaacat	ttgtggtctt	tatttacttt	60
gcttcgtgtg	tgggcacaaagc	aacatcttcc	ctaaatatat	attaccaaga	aaagcaagaa	120
gcagattagg	tttttgacaa	aacaaacagg	ccaaaagggg	gctgacctgg	agcagagcat	180
ggtagagaggc	aaggcatgag	agggcaagtt	tggtgtggac	agatctgtgc	ctactttatt	240
actggagtaa	aagaaaacaa	agttcattga	tgtcgaagga	tatatacagt	gtagaatt	300
a						301

&lt;210&gt; 285

<211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 285  
 acatcaccat gatcggtacc cccacccatt atacgttgta tgtttacata aatactcttc 60  
 aatgatcatt agtggtttta aaaaaatact gaaaactcct tctgcatccc aatctctaac 120  
 caggaaagca aatgctatct acagacctgc aagccctccc tcaaachaaa ctattctctgg 180  
 attaaatatg tctgacttct tttagaggtca cagcactagg caaatgctat ttacgatctg 240  
 caaaagctgt ttgaagagtc aaagccccc tgtgaacacg atttctggac cctgtaacag 300  
 t 301

<210> 286  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 286  
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60  
 tgtatattat ttttgccctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120  
 atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccaccca 180  
 aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240  
 gtttctgttc attgtgtatg cttcatcacc tatattaggg aaattccatt ttttcccttg 300  
 t 301

<210> 287  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 287  
 tacagatctg ggaactaaat attaaaaatg agtggtgctg gatatatgga gaatgttggg 60  
 cccagaagga acgtagagat cagatattac aacagctttg ttttgagggg tagaaatatg 120  
 aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc 180  
 ccgtgggtat ctctcccca gcttggtctg ctcagtgtat cacagtattc cattttgttt 240  
 gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300  
 t 301

<210> 288  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 288  
 gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60  
 agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa 120  
 gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180  
 aaagcatct gcttttgtga ttttaatttag ctcactctgg cactggaaga atccaaacag 240  
 tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300  
 a 301

<210> 289  
 <211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 289

```
ggtacactgt ttccatgta tgtttctaca cattgctacc tcagtgtcc tggaaactta      60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg    120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa    180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggg ggcggcgaan aagagaaaga    240
tgtgttttgt tttggactct ctgtggtccc ttccaatgct gtgggtttcc aaccagnnga    300
a                                     301
```

<210> 290

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 290

```
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac      60
tgactgatct gttcatttct ctcacagctc ttacccccaa aagcttttcc accctaagtg    120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg    180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc    240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagttag    300
a                                     301
```

<210> 291

<211> 301

<212> DNA

<213> Homo sapien

<400> 291

```
caggtaccaaa tttcttctat cctagaaaca tttcatttta tggtgttgaa acataacaac      60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc    120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagttcaat    180
agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa    240
acatgagctt cacttcccca ctaactaatt agcatctgtt atttcttaac cgtaatgcct    300
a                                     301
```

<210> 292

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 292

```

accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc      60
tgtattaaat aatttttaag tttaaaagat aaaataccat catttttaaat gttggtattc      120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg      180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc      240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa      300
a                                                                                   301

```

```

<210> 293
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 293
ggtaccaagt gctggtgccg gcctgttacc tgttctcact gaaaagtctg gctaattgctc      60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt      120
aacacaaaag tcactagcaa agtagcaaca gcttttaagtc taaatacaaa gctgttctgt      180
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg      240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gtcgagcat      300
g                                                                                   301

```

```

<210> 294
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 294
tgaccataaa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag      60
attcaataaaa attaccttta ttcacacatc tcaaaaacat tctgcaaatt cttagtgaag      120
tttaactata gtcacaganc ttaaataatc acattgtttt ctatgtctac tgaaaataag      180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc      240
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt      300
t                                                                                   301

```

```

<210> 295
<211> 305
<212> DNA
<213> Homo sapien

```

```

<400> 295
gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta      60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttgat aatccatctt gctttttccc cattggaact agtcattaac ccactctctga      180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacagggtga attggatggt      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt      300
tctct                                                                                   305

```

```

<210> 296
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 296
agggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct      60

```



```

cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg      120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac      180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt      240
tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg      300
c                                                                                   301

```

<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

```

actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta      60
aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga      120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt      180
tccatcattg ggagtgact ggccatccct caaaatttgt ctgggctggc ctgagtggtc      240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgcg      300

```

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

```

tatgggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc cccctccgcg      60
ggcatctgag agacctggtg ttccagtgtt tctggaatg ggtcccagtg ccgccggctg      120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccaccct      180
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta      240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg      300
t                                                                                   301

```

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

```

gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc      60
tactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc      120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg      180
gagtttcgcc atgttggcc gctgggtctca aactcctgac ctcaagcgac ctgcctgcct      240
cggcctccca aagtgtctgga attataggca tgagtcaaca cgcccagcct aaagatattt      300
t                                                                                   301

```

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

<400> 300  
 attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60  
 tatgtccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120  
 gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta 180  
 gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggttac 240  
 tataaagcct gcctctaaca gtccttgctt cttcacacca atcccagagc catcccccat 300  
 g 301

<210> 301  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 301  
 ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60  
 agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120  
 gggaactcac aaagaccctc agagctgaga caccacacac agtgggagct cacaaagacc 180  
 ctgagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240  
 cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300  
 t 301

<210> 302  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 302  
 aggtacacat ttagcttggt gtaaatgact cacaaaactg attttaaaat caagttaatg 60  
 tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac 120  
 ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180  
 ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240  
 caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg 300  
 g 301

<210> 303  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 303  
 aggtaccaac tgtggaaata ggtagaggat cattttttct ttccatatca actaagttgt 60  
 atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac 120  
 tggctaattg aactaccgct tgcagttaa aaatgggtgg ttgtgaaatg atcataggcc 180  
 agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240  
 catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac 300  
 c 301

<210> 304  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 304  
 acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaata 60  
 tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc 120  
 ctttttagtg tatcatatca ggaatcatct cacattgggt ttgtgccatta ctggtgcagt 180  
 gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga 240

ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct 300  
c 301

<210> 305  
<211> 301  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 305  
gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag 60  
cagggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggcg 120  
taaaggagga gaaacagata caaatctcc aactcagat taaggattc tcatgcctag 180  
aatattggta gaaacaagaa tacattcata tggcaataa ctaaccatgg tggaacaaaa 240  
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag 300  
a 301

<210> 306  
<211> 8  
<212> PRT  
<213> Homo sapien

<400> 306  
Val Leu Gly Trp Val Ala Glu Leu  
1 5

<210> 307  
<211> 637  
<212> DNA  
<213> Homo sapien

<400> 307  
acaggggratg aagggaaagg gagaggatga ggaagccccc ctggggattt ggtttgggcc 60  
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa ataggggcac 120  
attgaggaat gatacttgag ccaaagagc attcaatcat tgttttattt gccttmtttt 180  
cacaccattg gtgagggagg gattaccacc ctggggttat gaagatggtt gaacacccca 240  
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga 300  
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg 360  
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga 420  
tttcggtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtga 480  
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca 540  
ggtgggagcc tttcccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg 600  
ttacagatac tggggcagca aataaaactg aatcttg 637

<210> 308  
<211> 647  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(647)  
<223> n = A,T,C or G

&lt;400&gt; 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccaccctct	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
cattttgtgt	gtggataaa	tcaggatgcc	caggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	tttttctcct	gcttctgact	tgataaaaag	ggaccgt		647

&lt;210&gt; 309

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcattcatttt	tggccagcag	ttgtttgatc	180
accaaaccatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctggggtggt	ggagcgaaac	cgctactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttggt	tttgcctttc	ggtgtgtaag	attccttaagt			460

&lt;210&gt; 310

&lt;211&gt; 539

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagatttggt	ggaaatgggt	tggtttggtg	tatggtagtg	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaagggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

&lt;210&gt; 311

&lt;211&gt; 526

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(526)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; .311

caaatttgag	ccaatgacat	agaattttac	aatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaacc	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tgttcagcat	gaaatattag	ctacagggga	agctaaataa	180

attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg 240  
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa 300  
aaaatgggga aactctgaag gggttttaagt atcttacctg aagctacaga ctccataacc 360  
tctctttaca gggagctcct gcagccccta cagaaatgag tggtctgagat tcttgattgc 420  
acagcaagag cttctcatct aaacccttcc cctttttagt atctgtgtat caagtataaa 480  
agttctataa actgtagtnt acttatttta atccccaaag cacagt 526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)... (500)

<223> n = A,T,C or G

<400> 312

cctctctctc cccaccccct gactctagag aactggggtt tctcccagta ctccagcaat 60  
tcatttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct 120  
ccatttctct ttccttcca cctgccagtt ttgctgactc tcaacttgct atgagtgtaa 180  
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg 240  
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atccccctct 300  
tgcagatgtc tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaatcct 360  
tgctaagtgt gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct 420  
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt 480  
tagtcttaat tatctattgg 500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)... (718)

<223> n = A,T,C or G

<400> 313

ggagatttgt gtggtttgca gccgaggag accaggaaga tctgcatggt gggaaggacc 60  
tgatgataca gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat 120  
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa 180  
gtagtacat gtttttgac atttccagcc cttttaata tccacacaca caggaagcac 240  
aaaagggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga 300  
gcctcgccct gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg 360  
ttccttaaag gatggcagga aaacagatcc tgttgtggat atttatttga acgggattac 420  
agatttgaaa tgaaatcaca aagtgaagcat taccaatgag aggaaaacag acgagaaaat 480  
cttgatggtt cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc 540  
aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg 600  
cgttatacca atcatttcta tttctacct caaacaagct gtngaataac tgacttacgg 660  
ttctnttggc ccacatttcc atnatccacc cntcntttt aannttantc caaantgt 718

<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

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gtttattttac attacagaaa aaacatcaag acaatgtata ctattttcaaa tatatccata    60
cataatcaaa tatagctgta gtacatgttt tcattgggtg agattaccac aaatgcaagg    120
caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa    180
gctctcggta gtccagccac tgtgaaacat gtcaccttta gattaacctc gtggacgctc    240
ttgttgatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgc    300
tctggggcat ttccttgatga tgcagaggac caccacacag atgacagcaa tctgaatt    358

```

&lt;210&gt; 315

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 315

```

taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc    60
ataggtagtg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt    120
gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag cccaatgac    180
agtcaccagc tccccgacca gccggatata gtccttaggg gtcattgtagg cttcctgaag    240
tagcttctgc tgtaagaggg tggtgtcccg ggggctcgtg cgggtattgg tctgaggctt    300
gagggggcgg tagatgcagc acatggtgaa gcagatgatg t                    341

```

&lt;210&gt; 316

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 316

```

agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta    60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact    120
cattcaggga gctctggttg caatattagt t                    151

```

&lt;210&gt; 317

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 317

```

agaactagtg gatcctaata aaataacctga aacatatatt ggcatttatc aatggctcaa    60
atcttcattt atctctggcc ttaaccctgg ctcttgaggc tgcggccagc agatcccagg    120
ccagggtctt gttcttgcca cactgcttg a                    151

```

&lt;210&gt; 318

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 318

```

actggtggga ggcgctgttt agttggctgt ttccagaggg gtctttcgga gggacctcct    60
gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg    120
tgggggcggg ttatcaggca gtgataaaca t                    151

```

&lt;210&gt; 319

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 319

```

aactagtggg tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta    60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg    120

```

taagattggg tttatgtgat tttagtgggt a 151

<210> 320  
<211> 150  
<212> DNA  
<213> Homo sapien

<400> 320  
aactagtga tccactagtc cagtgtggtg gaattccatt gtgttggggt tctagatcgc 60  
gagcggctgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120  
gagtgttcta cagcttacag taaataccat 150

<210> 321  
<211> 151  
<212> DNA  
<213> Homo sapien

<400> 321  
agcaactttg tttttcatcc aggttatattt aggccttagga tttcctctca cactgcagtt 60  
taggggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120  
tgcctctgag aaatcaaagt cttcatacac t 151

<210> 322  
<211> 151  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(151)  
<223> n = A,T,C or G

<400> 322  
atccagcadc ttctcctggt tcttgccctc ctttttcttc ttcttasatt ctgcttgagg 60  
tttgggcttg gtcagtttgc cacagggtt ggagatggtg acagtcttct ggcattcggc 120  
attgtgcagg gctcgcttca nacttccagt t 151

<210> 323  
<211> 151  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(151)  
<223> n = A,T,C or G

<400> 323  
tgaggacttg tktttctttt ctttatattt aatcctctta ckttgtaa atattgccta 60  
nagactcant tactaccag tttgtggtt twtgggagaa atgtaactgg acagttagct 120  
gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324  
<211> 461  
<212> DNA  
<213> Homo sapien

<220>

<221> misc\_feature  
 <222> (1)...(461)  
 <223> n = A,T,C or G

<400> 324  
 acctgtgtgg aatttcagct ttectcatgc aaaaggattt tgtatccccg gcctacttga 60  
 agaagtgggc agctaaagga atccagggtg ttgggtggac tgtaataacc tttgatgaaa 120  
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 <212> DNA  
 <213> Homo sapien

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 <213> Homo sapien

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<210> 327  
 <211> 220



&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 327

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Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
      20              25              30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
      35              40              45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
 50              55              60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65              70              75              80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
      85              90              95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
      100             105             110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
      115             120             125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
      130             135             140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145             150             155             160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
      165             170             175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
      180             185             190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
      195             200             205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
      210             215             220

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&lt;210&gt; 328

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 328

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atccgcagtg ggtgctgtca gccacacact gtttccagaa ctctacacc atcgggctgg      180
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&lt;210&gt; 329

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 329

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      20              25              30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
      35              40              45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
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<210> 330  
<211> 70  
<212> DNA  
<213> Homo sapien

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<210> 331  
<211> 22  
<212> PRT  
<213> Homo sapien

<400> 331  
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<210> 332  
<211> 2507  
<212> DNA  
<213> Homo sapien

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&lt;210&gt; 333

&lt;211&gt; 3030

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 333

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&lt;210&gt; 334

&lt;211&gt; 2417

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 334

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&lt;210&gt; 335

&lt;211&gt; 2984

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 335

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 <211> 147  
 <212> PRT  
 <213> Homo sapien

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 20 25 30  
 Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln  
 35 40 45  
 Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala  
 50 55 60  
 Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln  
 65 70 75 80  
 Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln  
 85 90 95  
 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala  
 100 105 110  
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn  
 115 120 125  
 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro  
 130 135 140  
 Ala Phe Trp  
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<210> 337  
 <211> 9  
 <212> PRT  
 <213> Homo sapien

<400> 337  
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 <212> PRT  
 <213> Homo sapien

<400> 338  
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 1 5

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 <211> 318  
 <212> PRT  
 <213> Homo sapien

<400> 339  
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		50					55					60				
Gly	Ala	Arg	Val	Tyr		Leu	Ala	Cys	Arg	Asp	Val	Glu	Lys	Gly	Glu	Leu
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Val	Ala	Lys	Glu	Ile	Gln	Thr	Thr	Thr	Gly	Asn	Gln	Gln	Val	Leu	Val	
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Arg	Lys	Leu	Asp	Leu	Ser	Asp	Thr	Lys	Ser	Ile	Arg	Ala	Phe	Ala	Lys	
			100					105					110			
Gly	Phe	Leu	Ala	Glu	Glu	Lys	His	Leu	His	Val	Leu	Ile	Asn	Asn	Ala	
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Gly	Val	Met	Met	Cys	Pro	Tyr	Ser	Lys	Thr	Ala	Asp	Gly	Phe	Glu	Met	
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His	Ile	Gly	Val	Asn	His	Leu	Gly	His	Phe	Leu	Leu	Thr	His	Leu	Leu	
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Leu	Glu	Lys	Leu	Lys	Glu	Ser	Ala	Pro	Ser	Arg	Ile	Val	Asn	Val	Ser	
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Ser	Leu	Ala	His	His	Leu	Gly	Arg	Ile	His	Phe	His	Asn	Leu	Gln	Gly	
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Glu	Lys	Phe	Tyr	Asn	Ala	Gly	Leu	Ala	Tyr	Cys	His	Ser	Lys	Leu	Ala	
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Val	Thr	Thr	Tyr	Ser	Val	His	Pro	Gly	Thr	Val	Gln	Ser	Glu	Leu	Val	
225				230					235						240	
Arg	His	Ser	Ser	Phe	Met	Arg	Trp	Met	Trp	Trp	Leu	Phe	Ser	Phe	Phe	
				245					250					255		
Ile	Lys	Thr	Pro	Gln	Gln	Gly	Ala	Gln	Thr	Ser	Leu	His	Cys	Ala	Leu	
			260					265					270			
Thr	Glu	Gly	Leu	Glu	Ile	Leu	Ser	Gly	Asn	His	Phe	Ser	Asp	Cys	His	
		275					280				285					
Val	Ala	Trp	Val	Ser	Ala	Gln	Ala	Arg	Asn	Glu	Thr	Ile	Ala	Arg	Arg	
	290					295					300					
Leu	Trp	Asp	Val	Ser	Cys	Asp	Leu	Leu	Gly	Leu	Pro	Ile	Asp			
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<210> 340
<211> 483
<212> DNA
<213> Homo sapien
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ctcctgctgc	aggctggagt	gtctttattc	ctggcgggag	accgcacatt	ccactgctga	180
ggttggtggg	gcggtttatc	aggcagtgat	aaacataaga	tgtcatttcc	ttgactccgg	240
ccttcaattt	tctctttggc	tgacgcacga	gtccgtggtg	tcccgatgta	actgaccctt	300
gctccaaacg	tgacatcact	gatgctcttc	tcgggggtgc	tgatggcccg	cttggtcacg	360
tgtctaatct	cgccattcga	ctcttgctcc	aaactgtatg	aagacacctg	actgcacggt	420
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ctg						483

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<212> DNA
<213> Homo sapien
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&lt;400&gt; 341

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gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca	180
attaatttaa taattttctga tgatggtttt atctgcagta atatgtatat catctattag	240
aattttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc	300
ctgattctta acattgtctt taatgaccac aagacaacca acag	344

&lt;210&gt; 342

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 342

acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac	60
caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca	120
cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg	180
accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact	240
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat ttttaattggc	300
aagtgccact gtggaagag ttctgtgtg tgctgaagtt ctgaagggca gtcaaattca	360
tcagcatggg ctgtttggg caaatgcaaa agcacaggtc tttttagcat gctggtctct	420
cccgtgtcct tatgcaata atcgtcttct tctaaatttc tcttaggctt cattttccaa	480
agttcttctt ggtttgtgat gtctttcttg ctttccatta attctataaa atagtatggc	540
ttcagccacc cactcttcgc cttagcttga ccgtgagttc cggctgccgc tg	592

&lt;210&gt; 343

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 343

ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt	60
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cttgtaactc tcctttctcc tttcttcccc tttctctgcc cgcttttccc atcctgctgt	180
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ctgactgcc aagggggtca gaacccagc aatcccttcc tttcactacc ttcttttttg	300
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaaggag	360
aaaccaccaa gctgaaaaaa aa	382

&lt;210&gt; 344

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 344

ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga	60
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gttttagggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca	180
agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc	240
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ccttcttatt atttgatcta gaaattgccc tctttttacc cctaccatga gccctacaaa	420
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gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa	536

&lt;210&gt; 345

&lt;211&gt; 251



&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 345

```

acctttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg      60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg      120
gcgtgggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga      180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg      240
gtgccatttc c                                     251

```

&lt;210&gt; 346

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(282)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 346

```

cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt      60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcaagtaca aattctggga      120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctcccgc accaaaaaat      180
agaaaaggctt tctatttcac tggcccaggt aggggggaag agagtaactt tgagtctgtg      240
ggtctcatth cccaaggtgc cttcaatgct catnaaaacc aa                               282

```

&lt;210&gt; 347

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(201)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 347

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acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca      60
taaatataac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa      120
tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt      180
tataaagaat ttttttttgt c                                     201

```

&lt;210&gt; 348

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 348

```

ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca      60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgccctg ggcaggcaga      120
aggagacact cccagcatgg aggagggttt atcttttcat cctaggtcag gtctacaatg      180
ggggaagggtt ttattataga actcccaaca gccacactca ctctgccac ccaccgatg      240
gcctgcctc c                                     251

```

&lt;210&gt; 349

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 349

taaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac	60
aacccttgag gatgccagag ctatgggtcc agaacatggg gtggtattat caacagagtt	120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt	180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca	240
actcctgggt t	251

&lt;210&gt; 350

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 350

ctggacactt tgcgagggct tttgctggct gctgctgctg cccgtcatgc tactcatcgt	60
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aaaaaaggac tacagtgttc tatacgttgt tcccgtcct gtacgatctt agtatgtctt	900
aatcgacag	908

&lt;210&gt; 351

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 351

ccagttatatt gcaagtggta agagcctatt taccataaat aatactaaga accaactcaa	60
gtcaaacctt aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca	120
cattaacttg attttaaaat cagwtttgyg agtcatttac cacaagctaa atgtgtacac	180
tatgataaaa acaaccattg tattcctggt tttctaaaca gtccataatt ctaacactgt	240
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gatctgtcca caacaaactt gccctctcat gccttgctc tcaccatgct ctgctccagg	360
tcagccccct tttggcctgt ttgttttgte aaaaacctaa tctgcttctt gcttttcttg	420
gtaatatata tttagggaag atgttgcttt gccacacac gaagcaaagt aa	472

&lt;210&gt; 352

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 352

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tgtggataag gccagggtcaa tggctgcaag catgcagaga aagagggtaca tcggagcgtg	120
caggctgcgt tccgtcctta cgatgaagac cacgatgcag tttccaaaca ttgccactac	180
atacatggaa agggaggggga agccaaccca gaaatgggct ttctctaata ctgggatacc	240
aataagcaca a	251

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 <212> DNA  
 <213> Homo sapien

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 gataaggcaa cttatacatt gacaatccaa atccaataca tttaaacatt tgggaaatga 240  
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 gggctcctaa tgtagt 436

<210> 354  
 <211> 854  
 <212> DNA  
 <213> Homo sapien

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 aaatacaaaa ggattgagaa tcatggtgtc taatgtataa aagacccagg aaacataaat 720  
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 cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc 840  
 acacgggatg tcag 854

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 <211> 676  
 <212> DNA  
 <213> Homo sapien

<400> 355  
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 atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg 180  
 gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccaccccttc 240  
 ctgttcttta taaggcacac tcataccaac acgatcctat tctgtggcaa gcttgccctt 300  
 ccctaatacag atggggttga gtaaggctca gaggttgcaga tgagggtgcag agacaatcct 360  
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 tcatctgcaa aataggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc 480  
 tttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt 540  
 ggtgtctcat ttgagtgtc tccagtgaca tgatcaagtc aatgagtaaa attttaaggg 600  
 attagatttt cttgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct 660  
 gcttaaagaa aaccag 676

<210> 356

<211> 574  
 <212> DNA  
 <213> Homo sapien

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 ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acagggaagg 420  
 agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctgggtctg 480  
 gatagacggc acaggagct cttaggtcag cgctgctggg tggaggacat tcttgagtcc 540  
 agctttgcag cctttgtgca acagtacttt ccca 574

<210> 357  
 <211> 393  
 <212> DNA  
 <213> Homo sapien

<400> 357  
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 aagccacaac caaracttga ttttatcaac aaaaaccctt aaatataaac ggsaaaaaag 180  
 atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara 240  
 araarataag tgttatatgg aaagaagggc attcaagcac actaaaraaa cctgaggkaa 300  
 gcataatctg taaaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct 360  
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<210> 358  
 <211> 630  
 <212> DNA  
 <213> Homo sapien

<400> 358  
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 gcatagagta gggaagctaa tccagcacag ggaggtcaca gagacatccc taaggagtgc 180  
 gagtttaaac tgagagaagc aagtgtctaa actgaaggat gtgttgaaga agaagggaga 240  
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 attaaagatg tgaagattaa gatcttggtg gcattcaggg attggcactt ctacaagaaa 420  
 tcaactgaagg gagtaatgtg acattacttt tcacttcagg atggccattc taactccagg 480  
 gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcgatagt 540  
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 caagccagag gttcctccac aacaaccagt 630

<210> 359  
 <211> 620  
 <212> DNA  
 <213> Homo sapien

<400> 359  
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 ctaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat 180  
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aggattaact gtttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac      300
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tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt      420
aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca      480
aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca      540
aacaaaaagc tcacaccaa caaaaccatc aacttatttt gtattctata acatacgaga      600
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<210> 360

<211> 431

<212> DNA

<213> Homo sapien

<400> 360

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tactcatcat ttttggccag cagttgtttg atcaccaaac atcatgccag aatactcagc      180
aaaccttctt agctcttgag aagtcaaagt ccgggggaat ttattcctgg caattttaat      240
tggaactcct atgtgagagc agcggctacc cagctggggg ggtggagcga acccgtcact      300
agtggacatg cagtggcaga gtccttggtg accacctaga ggaatacaca ggcacatgtg      360
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agattcttag t

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<210> 361

<211> 351

<212> DNA

<213> Homo sapien

<400> 361

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ttgggtcttc tggctctttg ccaagtttcc cagccactcg agggagaaat atcgggaggt      180
ttgacttctt ccggggcttt cccgagggct tcaccgtgag ccctgcggcc ctcaagggtg      240
caatcttga ttcaatgtct gaaacctcgc tctctgectg ctggacttct gagggcgtca      300
ctgccactct gtctccagc tctgacagct cctcatctgt ggtcctgttg t

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<210> 362

<211> 463

<212> DNA

<213> Homo sapien

<400> 362

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ccccggtcac agaaatgacc aggttgggtg ttttcagggt ccagtgcctg gtcagcagct      180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttcctt ttcttcccca      240
gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttcttgggtg tgtttcttgt      300
agttccattt ctcaactttg ttgatctggg tgccttccat gtgctggctc tgggcatagc      360
cacacttgca cacattctcc ctgataagca cgatggtgtg gacaggaagg aaggatttca      420
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<210> 363

<211> 653

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

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&lt;223&gt; n = A,T,C or G

&lt;400&gt; 363

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atcttgagga tccntgggtc agaattccat ttaccttctg ggccagatac caccagaatg      600
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&lt;210&gt; 364

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 364

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aagtggatgc gcggaaaatg aaatcttctt caatagccca g          401

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&lt;210&gt; 365

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 365

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ccagtgtcat atttgggctt aaaatttcaa gaagggcact tcaaatggct ttgcatttgc      60
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gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga      300
acattcggca atgtccctt ttagccagat ttcttcttcg agtcccggga gagcag          356

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&lt;210&gt; 366

&lt;211&gt; 1851

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 366

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tcatcaccat tgccagcagc ggcaccgtta gtcagggttt ctgggaatcc cacatgagta      60
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tcaacttctt taagcctttg tgactcttcc tctgatgtca gctttaagtc ttgttctgga      180
ttgctgtttt cagaagagat ttttaacatc tgtttttctt tgtagtcaga aagtaactgg      240
caaattacat gatgatgact agaaacagca tactctctgg cgtcttttcc agatcttgag      300
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tgattaaaaa tttcaccact tgctgttttt gtcctgtgat accaagtagc agtgggtgtga      480
ggccatgctt gttttttgat tcgatatcag caccgtataa gagcagtgct ttggccatta      540

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&lt;210&gt; 367

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 367

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gcaatgatcc	atgtaactgc	aaacactgaa	tagcctgcta	ttactctgcc	ttcaaaaaaa	660
aaaaaaaa						668

&lt;210&gt; 368

&lt;211&gt; 1512

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 368

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&lt;210&gt; 369

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 369

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&lt;210&gt; 370

&lt;211&gt; 2184

&lt;212&gt; DNA



&lt;213&gt; Homo sapien

&lt;400&gt; 370

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tgtagtccca gctactcagg argctgaggc aggagaatgg catgaaccgc ggaggtggag     2100
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&lt;210&gt; 371

&lt;211&gt; 1855

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1855)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 371

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&lt;210&gt; 372

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 372

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&lt;210&gt; 373

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 373

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&lt;210&gt; 374

&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 374

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 <211> 2040  
 <212> DNA  
 <213> Homo sapien

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<210> 376  
 <211> 329  
 <212> PRT  
 <213> Homo sapien

<400> 376  
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 Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser  
 35 40 45  
 Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg  
 50 55 60

Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val  
 65 70 75 80  
 Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val  
 85 90 95  
 Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr  
 100 105 110  
 His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp  
 115 120 125  
 Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp  
 130 135 140  
 Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser  
 145 150 155 160  
 Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys  
 165 170 175  
 Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala  
 180 185 190  
 Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly  
 195 200 205  
 Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr  
 210 215 220  
 Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr  
 225 230 235 240  
 Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu  
 245 250 255  
 Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys  
 260 265 270  
 Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu  
 275 280 285  
 Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu  
 290 295 300  
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu  
 305 310 315 320  
 Ser Met Leu Phe Leu Val Ile Ile Met  
 325

&lt;210&gt; 377

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(148)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 377

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 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys  
 35 40 45  
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu  
 50 55 60  
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp  
 65 70 75 80  
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp  
 85 90 95

Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro  
 100 105 110  
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp  
 115 120 125  
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser  
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 Lys Asn Lys Val  
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 <212> PRT  
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 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
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 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
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 195 200 205  
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 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val







1265                      1270                      1275                      1280  
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr  
                                  1285                      1290                      1295  
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp  
                                  1300                      1305                      1310  
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Gly Val  
                                  1315                      1320                      1325  
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala  
                                  1330                      1335                      1340  
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala  
 1345                      1350                      1355                      1360  
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn  
                                  1365                      1370                      1375  
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr  
                                  1380                      1385                      1390  
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr  
                                  1395                      1400                      1405  
 Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu  
                                  1410                      1415                      1420  
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly  
 1425                      1430                      1435                      1440  
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Ser Gln Glu Pro Glu Ile Asn  
                                  1445                      1450                      1455  
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser  
                                  1460                      1465                      1470  
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly  
                                  1475                      1480                      1485  
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu  
                                  1490                      1495                      1500  
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
 1505                      1510                      1515                      1520  
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser  
                                  1525                      1530                      1535  
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu  
                                  1540                      1545                      1550  
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
                                  1555                      1560                      1565  
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
                                  1570                      1575                      1580  
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 1585                      1590                      1595                      1600  
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
                                  1605                      1610                      1615  
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro  
                                  1620                      1625                      1630  
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
                                  1635                      1640                      1645  
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile  
                                  1650                      1655                      1660  
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 1665                      1670                      1675                      1680  
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
                                  1685                      1690                      1695  
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr  
                                  1700                      1705                      1710  
 Met Lys His Gln Ser Gln Leu  
                                  1715

<210> 379  
 <211> 656  
 <212> PRT  
 <213> Homo sapien

<400> 379  
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415

Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
                   420                  425                  430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
                   435                  440                  445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
                   450                  455                  460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
 465                  470                  475                  480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
                   485                  490                  495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu  
                   500                  505                  510  
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys  
                   515                  520                  525  
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly  
                   530                  535                  540  
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser  
 545                  550                  555                  560  
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr  
                   565                  570                  575  
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln  
                   580                  585                  590  
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln  
                   595                  600                  605  
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys  
                   610                  615                  620  
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile  
 625                  630                  635                  640  
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu  
                   645                  650                  655

&lt;210&gt; 380

&lt;211&gt; 671

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 380

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1                  5                  10                  15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
                   20                  25                  30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
                   35                  40                  45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
                   50                  55                  60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65                  70                  75                  80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
                   85                  90                  95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
                   100                  105                  110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
                   115                  120                  125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
                   130                  135                  140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145                  150                  155                  160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala



625		630		635		640
Glu Lys Asp Ile Leu	His Glu Asn Ser Thr	Leu Arg Glu Glu Ile	Ala			
	645		650		655	
Met Leu Arg Leu Glu	Leu Asp Thr Met Lys His Gln Ser Gln	Leu				
	660		665		670	

<210> 381  
 <211> 251  
 <212> DNA  
 <213> Homo sapien

<400> 381  
 ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60  
 ggtaacatgc ttcccctaag ggtatcccaa ccaggggcc tcaccatgac ctctgagggg 120  
 ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggacca ggactcacac 180  
 atcctggggc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa 240  
 caagcagtca g 251

<210> 382  
 <211> 3279  
 <212> DNA  
 <213> Homo sapiens

<400> 382  
 cttcctgcag ccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60  
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120  
 cactgggagg ggacatcctg cagaaggtag gagtgagcaa acaccgctg caggggaggg 180  
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240  
 gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagttag ggatcagggg 300  
 cagggcgcga gatggcctca cacagggaag agaggggccc tctgcaggg cctcacctgg 360  
 gccacaggag gacactgctt ttcctctgag gagtcaggag ctgtggatgg tgctggacag 420  
 aagaaggaca gggcctggct cagggtgtcca gaggtgtcgt ctggcttccc tttgggatca 480  
 gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg 540  
 gtggctccag gccttgcccc tgccctggggc ctcaccagc ctcctcaca gtctcctggc 600  
 cctcagtctc tccctccac tccatctcc atctggcctc agtgggtcat tctgatcact 660  
 gaactgacca taccagccc tgcccacggc cctccatggc tcccacatgc cctggagagg 720  
 ggacatctag tcagagagta gtcctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780  
 gcacctgca gatggctccg gccctcatcc tgctgacctg tctgcaggga ctgtcctcct 840  
 ggaccttgcc ccttgtgcag gagctggacc ctgaagtccc ctcccatag gccaagactg 900  
 gagccttggt cctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960  
 catttctgtc tgttcttgag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020  
 agagatggag ttgcctaggc agttattggg gccaatctt ctcactgtgt ctctcctcct 1080  
 ttacccttag ggtgattctg ggggtccact tgtctgtaat ggtgtgcttc aaggatcac 1140  
 atcatggggc cctgagccat gtgccctgcc tgaaaagcct gctgtgtaca ccaagggtgt 1200  
 gcattaccgg aagtggatca aggacacat cgcagccaac cctgagtgc cctgtcca 1260  
 cccctacctc tagtaaat t aagtccact cacgttctgg catcacttg cctttctgga 1320  
 tgctggacac ctgaagcttg gaactcacct ggcgaagct cgagcctcct gactcctact 1380  
 gacctgtgct ttctggtgtg gagtccaggg ctgctaggaa aaggaaatgg cagacacagg 1440  
 tgtatgcaa tgttctgaa atgggtataa ttctgctcct tccttcggaa cactggctgt 1500  
 ctctgaagac ttctcgctca gtttcagtga ggacacac aaagacgtgg gtgacctgt 1560  
 tgtttggtgg gtgcagagat gggaggggtg gggccaccc tggaagagt gacagtga 1620  
 caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680  
 acacacagca aggttgacgc tgtaaacata gccacgctg tctggggggc actgggaagc 1740  
 ctagataagg cgtgagcag aaagaagggg aggatcctcc tatgttggtg aaggagggac 1800  
 tagggggaga aactgaaagc tgattaatta caggagggtt gttcaggtcc cccaaaccac 1860  
 cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920  
 ttattatggt ttgttacatt gataggatac atactgaaat cagcaacaa aacagatgta 1980  
 tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040

```

tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgatac cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgatacctta 2280
gtgtccagggt tttttactgg ggggtctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcttc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacaggga ttcatcacia atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaatgtc 2520
atctcccagg agttattcaa ggggtgagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggtctgc tgagtcaacc tttttattgta caggggatga gggaaagggg gaggatgagg 2640
aagccccctt ggggatttgg tttgggtctg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattgggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacatc agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggattgg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagttttt 3279

```

&lt;210&gt; 383

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
          5                      10                      15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20                      25                      30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35                      40                      45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50                      55                      60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65                      70                      75                      80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
          85                      90                      95

```

```

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
          100                     105                     110

```

```

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
          115                     120                     125

```

```

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
          130                     135                     140

```

```

Ala Leu Glu Arg Gly His Leu Val Arg Glu
          145                     150

```

<210> 384  
<211> 557  
<212> DNA  
<213> Homo sapiens

<400> 384  
ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60  
aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120  
ggggaagggt cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggg 180  
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgatc tacagctagg 240  
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300  
ctctgtagag agcagcattc ccagggaacct tggaaacagt tggcactgta aggtgcttgc 360  
tcccgaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420  
ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480  
tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540  
aaaaaaaaaa aaaaaaa 557

<210> 385  
<211> 337  
<212> DNA  
<213> Homo sapiens

<400> 385  
ttcccagggtg atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60  
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120  
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180  
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240  
tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300  
ctttggccac caattcccc ttttccacat cccggca 337

<210> 386  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 386  
gggcccgtcta cgggccaggg ccccgccctcg cgagtccctc tccccgggtg cctgcccgcga 60  
gccgcgtcgg ccagaggggt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120  
gcgaccttg cccgaaggct cttagcaagg cccaccgacc ccagccgcgg cggcggcggc 180  
gcggaactttg cccggtgtgt ggggcgggagc ggactgcgtg tccgcggacg ggcagcgaag 240  
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387  
<211> 537  
<212> DNA  
<213> Homo sapiens

<400> 387  
gggcccagtc gggcaccaag ggactctttg caggcttcc tctcggatc atcaaggctg 60  
ccccctctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120  
tgaaccagga ccggtctctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180  
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttctc agcactgagg 240  
gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggtg gtccctctgg 300  
gcggcccagc acttcctcag acacaacttc ttcctgctgc tccagtcgtg gggatcatca 360  
cttaccacc ccccaagttc aagaccaaat cttccagctg ccccttctgt gtttccctgt 420  
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480  
ctgacccttg ttaattcctt aagtctaaa atgatgaact tcaaaaaaaaa aaaaaaa 537

<210> 388  
<211> 520  
<212> DNA  
<213> Homo sapiens

<400> 388  
aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60  
tgagggttaaa ccagtttgca ttcccctaata gtggaaaaag taagaggact actcagcact 120  
gtttgaagat tgctcttctt acagcttctg agaatttgtt tatttcactt gccaaagtga 180  
ggacccccctc cccaacatgc ccagcccac ccctaagcat ggtcccttgt caccaggcaa 240  
ccaggaaact gctacttggtg gacctcacca gagaccagga gggtttggtt agctcacagg 300  
acttccccca cccagaaga ttagcatccc atactagact cataactaac tcaactaggc 360  
tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctgggttatta taaacagaaa 420  
atctttcttc ttctcattac cagtaaaggc tcttggtatc tttctggttg aatgatttct 480  
atgaacttgt cttatttttaa tgggtgggtt ttttctggt 520

<210> 389  
<211> 365  
<212> DNA  
<213> Homo sapiens

<400> 389  
cggtgccccca gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60  
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtggtgccct ctgctccccc 120  
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180  
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgctctcac agctgagact 240  
cccaggaaac cttcagacta ccttctcttg ccttcagcaa ggggcgttgcc ccacattctc 300  
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360  
gggag 365

<210> 390  
<211> 221  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(221)  
<223> n = A,T,C or G

<400> 390  
tgctctcca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60  
tacacggntt ctcatgggtg tggaacatct ctgcttgcg tttcaggaag gcctctggct 120  
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaaagg cggagcttat 180  
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

<210> 391  
<211> 325  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(325)  
<223> n = A,T,C or G

<400> 391



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tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttn gat ntccanagcc ctacccaten tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgcag tctctaccta ccagtacgat 300
gagacctccg gctactacta tgacc 325
```

<210> 392

<211> 277

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(277)

<223> n = A,T,C or G

<400> 392

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atattgttta actccttcct ttatatcttt taacattttc atggngaaag gttcacatct 60
agtctcactt nggcnagn gn ctctacttg agtctcttcc ccggcctggn ccagtnghaa 120
antaccanga accgncatgn cttaanaacn ncctggtttn tgggttnntc aatgactgca 180
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggagg 240
ctgaggatac agcgccgcgt cctgtgttgc tgggggaa 277
```

<210> 393

<211> 566

<212> DNA

<213> Homo sapiens

<400> 393

```
actagtcacag tgtgggtggaa ttcgcgcccg cgtegcagga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga tttaaattcag cctaaacggt 120
ttgcggggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggtct agtttgtcca tcagcattat catgatatac ggactgggta cttgggttaag 240
gaggggtcta ggagatctgt cctttttaga gacaccttac ttataatgaa gtatttggga 300
gggtgggtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcccttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa 566
```

<210> 394

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

```
gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaccgggcca aggcctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggttttaa ggagttttaa gctgagtgtc actgtagacc ccaaatacca 180
tccaagatt atcggggagaa agggggcagc aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag gtagtctata ctgagaattg tgggtgaact 360
```

tgagcagatg gtttctgagg acgt

384

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcattct ctcactacag acctctgacc atgggacggg 360
gcagcctggt gagaccatcc aatcccaaat aaaatgcac 399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtggag gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgtagt gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

```
actagtnca gttggtggaa ttgcggcccg cgtcgacctc naanccatct ctatagcaaa 60
tccatccccg ctctggttg gtnacagaat gactgacaaa 100
```

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398  
gcgggcgcgt cgacagcagt tccgccageg ctcgcccctg ggtggggatg tgctgcacgc 60  
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120  
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180  
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240  
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399  
<211> 298  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(298)  
<223> n = A,T,C or G

<400> 399  
acggagggtg aggaagcgn cctgggatcg anaggatggg tcttgn catt gaccncctcn 60  
gggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120  
cggagatcga gcgcattggc ctggtcatgg accgcatggg ctccgtggag cgcattgggct 180  
ccggcattga gcgcattggc ccgctgggccc tcgaccacat ggctccanc attgancgca 240  
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcattggg 298

<210> 400  
<211> 548  
<212> DNA  
<213> Homo sapiens

<400> 400  
acatcaacta cttcctcatt ttaaggatg gcagttccct tcateccett ttctgcctt 60  
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaagg 120  
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180  
tgagtctctt tttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240  
tgacagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatcccg 300  
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360  
gttgggccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420  
ctttccagt atctcctacc atgggcccc ctctgggat caagcccctc ccaggccctg 480  
tcccagccc ctctgcccc agcccaccg cttgccttg tgctcagccc tcccattggg 540  
agcagggt 548

<210> 401  
<211> 355  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(355)  
<223> n = A,T,C or G

<400> 401  
actgtttcca tggtatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60  
tgatgtctcc aagtagtcca cttcatttta actctttgaa actgtatcat ctttgccaag 120  
taagagtggg ggcctatctc agctgctttg acaaaatgac tggtcctga cttaacgttc 180  
tataaatgaa tgtgtggaag caaagtgcc atgggtggcg cgaagaagan aaagatgtgt 240  
ttgtttttg actctctgtg gtccttcca atgctgnggg tttccaacca ggggaagggt 300

ccctttttgca ttgccaaagt ccataaccat gagcactact ctacccatggn tctgc 355

<210> 402

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 402

```
atgggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
aatggaaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
ttgtggagct tctcccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc cttttctgaa gttttactca ttccaa 407
```

<210> 403

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 403

```
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcacccaa 60
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctgggc aatctacaaa 120
tagagaacaa gacctactca gtcatgaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
gga 303
```

<210> 404

<211> 225

<212> DNA

<213> Homo sapiens

<400>. 404

```
aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
attgttaatg cactcattta cctttacatg gtgaaagtcc tctcttgatc ctacaaacag 120
acattttcca ctctgttttc catagtgtt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225
```

<210> 405

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(334)

<223> n = A,T,C or G

<400> 405

```
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtecc tctccttact 120
tcacccccat cccatgccaa aggaagaccc tccctccttg gtcacagcc ttctctaggc 180
ttcccagtg ctcaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcanng tggatcccac ccct 334
```

<210> 406

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 406

```
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aattnnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216
```

<210> 407

<211> 413

<212> DNA

<213> Homo sapiens

<400> 407

```
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtgc tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagtccc agaaaaagt aaacagaca atgggccagg ttctgtagta aag 413
```

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncettaacta gttaatcctt aaagggctan ntaatectta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttctgggcta cccatgtact 180
ntt 183
```

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

```
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtgggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ctttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgntcctt gctggggggg 240
ggcctatgct                                     250
```

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

```
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccaggagacc ttggaaacag ttggcactgt aaggtgcttg ctccccaaga cacatcctaa 180
aaggtgttgt aatgggtgaaa accgcttcct tctttattgc ccttcttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaaag ttcaattgng aaaatgaata 300
tcntgc                                           306
```

<210> 411

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(261)

<223> n = A,T,C or G

<400> 411

```
agagatattn cttaggtnaa agttcataga gtteccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggngaggcaa a                                     261
```

<210> 412

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(241)

<223> n = A,T,C or G

<400> 412

```
gttcaatggt acctgacatt tctacaacac ccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tcaactgggtta cattgaattc ccaaactacc cangcaatta cccagccaac 240
a                                                                                   241
```

<210> 413

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 413

```
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtag cttctctttg ttgtgaaggga taatcaaact gaacaacaaa 120
aagtttactc tctctatttg gaacctaaaa actctcttct tcttgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t                   231
```

<210> 414

<211> 234

<212> DNA

<213> Homo sapiens

<400> 414

```
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggg cttccttttg catgggatgg ggatgaagta aggagagggg 180
ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca          234
```

<210> 415

<211> 217

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(217)

<223> n = A,T,C or G

<400> 415

```
gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cacttttctca 120
cacctagcaa tagtagaatt cagtcttact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc                               217
```

<210> 416

<211> 213

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature  
 <222> (1)...(213)  
 <223> n = A,T,C or G

<400> 416  
 atgcataatnt aaagganact gcctcgcttt tagaagacat ctggncctgct ctctgcatga 60  
 ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120  
 cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180  
 atattggaac agatggagtc tctactacaa aag 213

<210> 417  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(303)  
 <223> n = A,T,C or G

<400> 417  
 nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60  
 gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cacactggag 120  
 agaagccata caaatgcaat gagggtggga agagcttcag gagggattcc cattatcaag 180  
 ttcattctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt ggggaagggt 240  
 tcantcaaag ttctgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300  
 agt 303

<210> 418  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(328)  
 <223> n = A,T,C or G

<400> 418  
 tttttggcgg tgggtggggca gggacggggac angagtctca ctctgttgcc caggctggag 60  
 tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120  
 gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180  
 gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240  
 tcagnngtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300  
 aaagtgctan gattacaggc cgtgagcc 328

<210> 419  
 <211> 389  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(389)  
 <223> n = A,T,C or G

<400> 419  
 cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatag 60



```

acccttgagc catggactgg agcctgaaag gcagcgtaca ccttgctcct gatcttgctg 120
cttgtttcct ctctgtggct ccattcatag cacagttggt gactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcactcgct cccgcaaatt gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtctt ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

```

&lt;210&gt; 420

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 420

```

gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtccattga cacttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgcctatg acaaacctgg caagcccg 408

```

&lt;210&gt; 421

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (352)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 421

```

gctcaaaaat ctttttactg atnggcattg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggctt tttttgggtc cttcttctcc accacnata acttgagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacagggt tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttctt gg 352

```

&lt;210&gt; 422

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 422

```

atgccaccat gctggcaatg cagcgggcgg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcgg cgtcaatcct ggccaaggct agccgtgac 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggct 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337

```

&lt;210&gt; 423

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature  
<222> (1)...(310)  
<223> n = A,T,C or G

<400> 423  
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60  
aggagaatga ggcctggcct gggagccctg tgccactan aagcncatta gattatccat 120  
tactgacag aacagggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180  
tccttcttga agattctttg gcagttgtct ttgtcataac ccacagggtg anaaacaagg 240  
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300  
tccgagttta 310

<210> 424  
<211> 370  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(370)  
<223> n = A,T,C or G

<400> 424  
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60  
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120  
cactgacaga acagggtctt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180  
ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacagggtga gaaacatcct 240  
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300  
cacgaagggt gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360  
tccgtcgacg 370

<210> 425  
<211> 216  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(216)  
<223> n = A,T,C or G

<400> 425  
aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaataga 60  
taacaacnca acatcaagg n aaananaaca ggaatggntg actntgcata aatnggccga 120  
anattatcca ttatnttaag ggttgacttc agntacagc acacagacaa acatgcccgag 180  
gaggntntca ggaccgctcg atgtnttntg aggagg 216

<210> 426  
<211> 596  
<212> DNA  
<213> Homo sapiens

<400> 426  
cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60  
tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120  
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180  
gctgtccttg tattttgatt aacctaattg ccttcccagc acgactcgga ttcagctgga 240  
gacatcacgg caacttttaa tgaaatgatt tgaagggcc a ttaagaggca cttcccgtta 300

```

ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcaactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgctgg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

```

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

```

gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
cccgaggagca gccttanaga gctcctgttt gactgcccg ctcagng 107

```

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

```

gaacttcna anaangactt tattcactat tttacatt 38

```

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

```

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggg ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttcact tcagttacac ctcaactcacc atcctctcct gttggttctg tgetgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaaaa gtttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540
ttat 544

```

<210> 430

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(507)

<223> n = A,T,C or G

<400> 430

```

cttatcncaa tggggctccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccocgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaaagct gcccagaatg ttntcctggg cagcgttggtg atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtgaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa
507

```

<210> 431

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```

gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagattgg aaacaaaatc ccaggagttt tgtgtgtgga gtccctgggtt ttccaacaga 240
catcattcca gcattctgag attaggngga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggctttttac tctgctgttt ct
392

```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```

ggtatcnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtcaa gctctcggn a gtcagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt
387

```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 433

```
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gccactgggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281
```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```
ttttaaaata agcatttagt gctcagtcct tactgagtac tctttctctc cctcctctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatatattg 120
tggtgcaaaa aaaaaaagt gtctttgttt aaaattactt gggttgtagaa tccatcttgc 180
tttttcccca ttggaactag tcattaacct atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacctt ttcaccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaacct 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttta 484
```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```
gcgcccgtca gagcaggtea ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatacgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaaccct ctcctcgcgc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcattgggtc ggggtgacct 240
cttgagagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaaacctc ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424
```

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(667)

<223> n = A,T,C or G

<400> 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctactctt caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cggtaacgt ctgtgcttcg aatataaacc 360
```

```
tgttcatgtt tataggactc attcaagaat tttctatatc tctttcttat atactctcca 420
agttcataat gctgctccat gcccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaagggt tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttggtc agtacacttc ggtctagcca gaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag 667
```

&lt;210&gt; 437

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaa gctggattggc acactaggac tctaccatac cgggttttgt 120
taaaagctcag gttaggaggc tgataagctt ggaagggaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac cctcttgct tctactctct gccagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc 693
```

&lt;210&gt; 438

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 438

```
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgaggagg ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaa acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctggtgg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

&lt;210&gt; 439

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(431)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 439

```
gttcctnnta actcctgcc aaaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttggg gtttcggcat ggagaccgaa 180
gtccatttga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gattcctata aacatgaaca ggttttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgctga cgcggccgcg 420
aatttagtag t 431
```

<210> 440  
<211> 523  
<212> DNA  
<213> Homo sapiens

<400> 440  
agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60  
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120  
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180  
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240  
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300  
actggaaaac tgctactatc tgtttttata ttctgttaa aatatatgag gctacagaac 360  
taaaaaattaa aacctctttg tgcccttgg tccctggaaca tttatgttcc ttttaaagaa 420  
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480  
tatatatatc atagcaaata agtcacttga tgagaacaag cta 523

<210> 441  
<211> 430  
<212> DNA  
<213> Homo sapiens

<400> 441  
gttctctcta actcctgcca gaaacagctc tctcaacat gagagctgca cccctctccc 60  
tggccagggc agcaagcctt agccttggtc tcttgtttct gctttttttc tggctagacc 120  
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180  
gtcccatgga cacttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240  
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300  
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360  
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420  
aatttagtag 430

<210> 442  
<211> 362  
<212> DNA  
<213> Homo sapiens

<400> 442  
ctaaggaatt agtagtgttc ccatcacttg tttggagtgt gctattctaa aagattttga 60  
tttcttgga tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120  
cttcaacttc gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180  
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240  
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300  
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360  
tc 362

<210> 443  
<211> 624  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)... (624)  
<223> n = A,T,C or G

<400> 443  
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60

```

ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaaacttg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360
taacgcctac aaacactta aacatagata acatagggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tattttaaact 600
ttgtccctat ctgctaaaca gatc 624

```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```

gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgtg gtcagcaaata ccttgaatgc 180
tgcttaattgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcactctgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425

```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```

catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgct tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggtctctcc tcttgtattt tgaagcagtg 360
tggtgtgctgg attgataaaa aaaaaaaaaa tcgacgcggc cgcaatttta gtag 414

```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(631)



<223> n = A,T,C or G

<400> 446

```
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
atgctggtta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgacctg catttggtgg 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                     631
```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```
ccttgggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtga gtacacttcg gtcta                               585
```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```
tgctcgtggg tcattctgan nnccgaactg accntgcccag ccctgcccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag                                     93
```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

&lt;222&gt; (1)...(706)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 449

```

ccaagttcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggctcgggcg cgccccattc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc caggggttttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncacca 660
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&lt;210&gt; 450

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 450

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gcgaatttag tag 493

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&lt;210&gt; 451

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 451

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&lt;210&gt; 452

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<223> n = A,T,C or G

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<212> DNA  
<213> Homo sapiens

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<223> n = A,T,C or G

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<211> 231  
<212> DNA  
<213> Homo sapiens

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agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180  
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<213> Homo sapiens

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gttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180  
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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

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<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

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<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

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<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

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<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

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 <213> Homo sapiens

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&lt;210&gt; 469

&lt;211&gt; 2229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

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2229

&lt;210&gt; 470

&lt;211&gt; 2426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

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2426

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&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

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&lt;210&gt; 474

&lt;211&gt; 1594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 474

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aaaaaaaaaa aaaa 3434

```

Met	Asp	Gly	His	Thr	Asp	Ile	Trp	Arg	Asn	His	Met	Asp	Thr	Pro	Pro
				5					10					15	
His	Tyr	His	Arg	Asp	Thr	Asp	Thr	Arg	Arg	His	His	His	Met	Asp	Thr
			20					25					30		
Leu	Ser	His	Tyr	His	Arg	Asp	Thr	Arg	His	His	Thr	Val	Thr	Trp	Thr
		35					40					45			
His	His	His	Thr	His	Glu	His	Thr	Asp	Thr	Leu	Pro	Tyr	Gly	His	Trp
	50					55					60				
His	Thr	His	Cys	His	Thr	Val	Thr	Trp	Thr	His	Leu	His	Thr	Ile	Thr
65					70					75					80
Pro	Pro	His	Thr	Leu	Pro	Val	Asp	Thr	Arg	Thr	His	Arg	His	Cys	His
				85					90					95	
Thr	Asp	Thr	Gln	Asn	Thr	Val	Thr	Arg	Arg	His	His	His	Ala	Asp	Thr
			100					105					110		
Pro	Pro	Leu	Trp	Cys	Arg	Leu	Asn	Tyr	Pro	Ala	Gly	Gly	Thr	Ala	Val
		115					120					125			
Ala	Tyr	Ser	Cys	Leu	Ser	Asp	Trp	Leu	Ser	Pro	Gln				
130						135					140				

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<210> 478
<211> 143
<212> PRT
<213> Homo sapiens
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Met	Tyr	Arg	His	Thr	Glu	Thr	Leu	Pro	His	Gly	Asp	Thr	Val	Thr	Gln
				5					10					15	
Ser	His	Gly	His	Thr	Gly	Ile	Val	Thr	Trp	Thr	Asp	Thr	Gln	Thr	Tyr
			20					25					30		
Gly	Glu	Ile	Thr	Trp	Thr	His	His	His	Thr	Ile	Thr	Gly	Thr	Gln	Thr
		35					40					45			
His	Gly	Asp	Ile	Thr	Thr	Trp	Thr	His	Cys	His	Thr	Thr	Thr	Gly	Thr
	50					55					60				
Arg	Asp	Ile	Thr	Leu	Ser	His	Gly	His	Thr	Ile	Thr	His	Met	Asn	Thr
65					70					75					80
Pro	Thr	His	Cys	His	Met	Asp	Thr	Gly	Thr	His	Thr	Ala	Thr	Leu	Ser
				85					90					95	

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<210> 479
<211> 222
<212> PRT
<213> Homo sapiens
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<400> 479																	
Met	Tyr	Arg	His	Thr	Glu	Thr	Leu	Pro	His	Gly	Asp	Thr	Val	Thr	Gln		
				5					10						15		
Ser	His	Glu	His	Thr	Gly	Ile	Val	Thr	Trp	Thr	Asp	Thr	Gln	Thr	Tyr		
			20					25					30				
Gly	Glu	Ile	Thr	Leu	Thr	His	His	His	Thr	Ile	Thr	Gly	Thr	Gln	Thr		
		35					40					45					
His	Gly	Asp	Ile	Thr	Thr	Trp	Thr	His	Cys	His	Thr	Thr	Thr	Gly	Thr		
	50					55						60					
Arg	Asp	Ile	Thr	Leu	Ser	His	Gly	His	Thr	Ile	Thr	His	Met	Asn	Thr		
	65				70						75				80		
Pro	Thr	His	Cys	His	Met	Asp	Thr	Ala	Thr	His	Thr	Ala	Thr	Leu	Ser		
				85					90					95			
His	Gly	His	Thr	Ser	Ile	Pro	Ser	His	His	His	Thr	His	Cys	His	Val		
			100					105					110				
Asp	Thr	Arg	Thr	His	Arg	His	Cys	His	Thr	Asp	Thr	Gln	Asn	Thr	Val		
		115					120					125					
Thr	Arg	Arg	His	His	His	Ala	Asp	Thr	Pro	Pro	His	Gly	His	Ser	Thr		
	130					135					140						
Arg	His	Ser	Ala	Thr	Gln	Ile	His	His	His	Thr	Glu	Met	Arg	Thr	His		
	145				150					155					160		
Cys	His	Thr	Asp	Thr	Thr	Thr	Ser	Leu	Pro	His	Phe	His	Val	Ser	Ala		
				165					170					175			
Gly	Gly	Val	Gly	Pro	Thr	Thr	Leu	Gly	Ser	Asn	Arg	Glu	Ile	Thr	Trp		
			180					185					190				
Thr	Tyr	Ser	Glu	Gly	Lys	Ile	Phe	Phe	Tyr	Phe	Leu	Gly	Asn	Gln	Ala		
		195					200					205					
Arg	Leu	Cys	Leu	Lys	Lys	Arg	Lys	Lys	Lys	Gln	Tyr	Thr	Val				
	210					215						220					

<210> 480  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val  
                           5                          10                          15  
 Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr  
                           20                          25                          30  
 Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg  
                           35                          40                          45  
 Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly  
                           50                          55                          60  
 Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln  
                           65                          70                          75                          80  
 Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys  
                           85                          90                          95  
 Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly  
                           100                          105                          110  
 Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu  
                           115                          120                          125  
 Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly  
                           130                          135                          140

<210> 481  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

<400> 481  
 Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro  
                           5                          10                          15  
 Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg  
                           20                          25                          30  
 Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser  
                           35                          40                          45  
 Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys  
                           50                          55                          60  
 Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro



[illegible]

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<210> 482
<211> 143
<212> PRT
<213> Homo sapiens
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<400> 482
Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
      5                      10                      15

Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
      20                      25                      30

Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
      35                      40                      45

Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
      50                      55                      60

Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
      65                      70                      75                      80

Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
      85                      90                      95

Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
      100                      105                      110

Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
      115                      120                      125

Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
      130                      135                      140

```

```
<210> 483
<211> 143
<212> PRT
```

<213> Homo sapiens

<400> 483

```

Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
          5              10              15

Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
          20              25              30

Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
          35              40              45

Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
          50              55              60

Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
          65              70              75              80

Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
          85              90              95

Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
          100             105             110

Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
          115             120             125

Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
          130             135             140

```

<210> 484

<211> 30

<212> PRT

<213> Homo Sapien

<400> 484

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
  1          5              10              15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
          20              25              30

```

<210> 485

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 485

gggaagctta tcacctatgt gccgcctctg c

<210> 486

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 486

gcgaattctc acgctgagta tttggcc

27

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 487

cccgaattct tagctgccca tccgaacgcc ttcac

36

<210> 488

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 488

gggaagcttc ttccccggct gcaccagctg tgc

33

<210> 489

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 489

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala

1

5

10

15

Ser Val Ala

<210> 490

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 490

Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys

1

5

10

15

Leu Ser His Ser

20

<210> 491

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 491

Thr	Cys	Leu	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu
1				5					10					15	
Thr	Gly	Phe	Thr												
			20												

<210> 492

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 492

Ala	Leu	Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr
1				5					10					15	
Leu	Ala	Ser	Leu												
			20												

<210> 493

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 493

Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro
1				5					10					15	
Lys	Tyr	Arg	Gly												
			20												

<210> 494

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 494

Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala	Ser	Ser	Glu	Asp	Ser
1				5					10					15	
Leu	Met	Ile	Ser												
			20												

<210> 495

<211> 20

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 495

Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro  
1 5 10 15  
Phe Pro Asn Gly  
20

&lt;210&gt; 496

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 496

Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu  
1 5 10 15  
Pro Pro Pro Pro Ala  
20

&lt;210&gt; 497

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 497

Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val  
1 5 10 15  
Ser Val Arg Val  
20

&lt;210&gt; 498

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 498

Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val  
1 5 10 15  
Val Pro Gly Arg  
20

&lt;210&gt; 499

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Made in a lab

<400> 499

```
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 1           5           10           15
Ser Ala Phe Leu
                20
```

<210> 500

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 500

```
Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 1           5           10           15
Gly Ser Ile Val
                20
```

<210> 501

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 501

```
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
 1           5           10           15
Val Ser Ala Ala
                20
```

<210> 502

<211> 414

<212> DNA

<213> Homo Sapien

<220>

<221> misc\_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 502

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caccatggag acaggcctgc gctggctttt cctggctcgt gtgctcaaag gtgtccaatg      60
tcagtcggtg gaggagtccg ggggtcgcct ggtcacgcct gggacacctt tgacantcac      120
ctgtagagtt tttggaatng acctcagtag caatgcaatg agctgggtcc gccaggctcc      180
aggggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc      240
gaaaggccga ttnatnattt ccaaaacctn gaccacgggtg gatttgaaaa tgaccagtcc      300
gacaaccgag gacacggcca cctatttttg tggcagaatg aatactggta atagtggttg      360
gaagaatatt tggggcccag gcaccctggt caccgtntcc tcagggcaac ctaa          414
```

<210> 503

<211> 379

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 503

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ctgggtcacgc	ctgggacacc	cctgacactc	acctgcaccg	tntctggatt	ngacatcagt	120
agctatggag	tgagctgggt	ccgccaggct	ccagggaagg	ggctgggnata	catcggtatca	180
ttagtagtag	tggtacattt	tacgcgagct	gggcgaaagg	ccgattcacc	atttccaaaa	240
cctngaccac	gggtgatttg	aaaatcacca	gtttgacaac	cgaggacacg	gccacctatt	300
tntgtgccag	aggggggttt	aattataaag	acatttgggg	cccaggcacc	ctgggtcaccg	360
tntccttagg	gcaacctaa					379

<210> 504

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 504

Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp	Ser	Pro	Tyr	Phe	Lys	Glu
1			5					10					15		
Asn	Ser	Ala													

<210> 505

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 505

Lys	Glu	Asn	Ser	Ala	Phe	Pro	Pro	Phe	Cys	Cys	Asn	Asp	Asn	Val	Thr
1			5					10					15		
Asn	Thr	Ala	Asn												
			20												

<210> 506

<211> 407

<212> DNA

<213> Homo Sapien

<400> 506

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tcgttgagg	agtccggggg	tcgcctgggc	acgcctggga	caccctcgac	actcacctgc	120
accgtctctg	gattctccct	cagtagcaat	gcaatgatct	gggtccgcca	ggctccaggg	180
aaggggctgg	aatacatcgg	atacattagt	tatggtggta	gcgcatacta	cgcgagctgg	240
gtgaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgag	aatgaccagt	300
ctgacaaccg	aggacacggc	cacctatttc	tgtgccagaa	atagtgattt	tagtggtatg	360
ttgtggggcc	caggcaccct	ggtcaccgct	tcctcagggc	aacctaa		407

<210> 507  
 <211> 422  
 <212> DNA  
 <213> Homo Sapien

<400> 507  
 atggagacag gctcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60  
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 acagtctctg gattctccct cagcaactac gacctgaact gggtcgcca ggctccaggg 180  
 aaggggctgg aatggatcgg gatcattaat tatgttggtg ggacggacta cgcgaaactgg 240  
 gcaaaaggcc gggtcaccat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt 300  
 ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct 360  
 ggtccgtgct tgcgcatctg gggcccaggc accctgggtc ccgtctcctt agggcaacct 420  
 aa 422

<210> 508  
 <211> 411  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(411)  
 <223> n = A,T,C or G

<400> 508  
 atggagacag gctcgctg cttctcctgg tcgctgtgct caaaggtgtc cagtgtcagt 60  
 cggtggagga gtccgggggt cgcctgggtc cgcctgggac acccctgaca ctcacctgca 120  
 cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccaggga 180  
 aggggctgga atggatcgga atcattggtg ctctgtgtga cacatactac gcgaggtggg 240  
 cgaaaggccg attcaccatc tccaaaacct cgaccacggg gcatntgaaa atcnccagtc 300  
 cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta 360  
 ctggttatta taaaatctgg ggcccaggca ccctgggtcac cgtctccttg g 411

<210> 509  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 509  
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 1 5 10 15

<210> 510  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 510  
 Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile  
 1 5 10 15



<210> 511  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 511

Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys
1				5				10					15	

<210> 512  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 512

Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu
1				5				10					15	

<210> 513  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 513

Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Asx	Val	Tyr	Thr	Asn	Leu
1				5				10					15	

<210> 514  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 514

Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser
1				5				10					15	

<210> 515  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 515  
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg  
1 5 10 15

<210> 516  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 516  
Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln  
1 5 10 15

<210> 517  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 517  
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met  
1 5 10 15

<210> 518  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 518  
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
1 5 10 15

<210> 519  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 519  
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys  
1 5 10 15  
Gly

<210> 520  
<211> 25  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 520

Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr
1				5				10						15	
Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly							
			20				25								

&lt;210&gt; 521

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 521

Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
1				5				10						15	
Pro	Pro	Pro	Pro	Ala											
				20											

&lt;210&gt; 522

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 522

Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr	Gly	Ser	Gln	Glu	Asp
1				5					10					15	
Phe	Thr	Gln	Val												
			20												

&lt;210&gt; 523

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(254)

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 523

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5				10						15	
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
			20				25					30			
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35				40					45				

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln  
 50 55 60  
 Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly  
 65 70 75 80  
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met  
 85 90 95  
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu  
 100 105 110  
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu  
 115 120 125  
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala  
 130 135 140  
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg  
 145 150 155 160  
 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu  
 165 170 175  
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys  
 180 185 190  
 Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly  
 195 200 205  
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly  
 210 215 220  
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu  
 225 230 235 240  
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 245 250

&lt;210&gt; 524

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 524

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 ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagcccgcac 120  
 tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgctctg 180  
 gtgcattccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg 240  
 ctggggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggg ggaggccagc 300  
 ctctccgtac ggcacccaga gtacaacaga cccttgctcg ctaacgacct catgctcatc 360  
 aagttggacg aatccgtgtc cgagtctgac accatccgga gcattcagcat tgcttcgcag 420  
 tgcctaccg cggggaactc ttgcctcgtt tctggctggg gtctgctggc gaacggcaga 480  
 atgcctaccg tgcctcagtg cgtgaacgtg tcgggtggtg ctgaggaggt ctgcagtaag 540  
 ctctatgacc cgctgtacca cccagcatg ttctgcgccg gcggagggca agaccagaag 600  
 gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 660  
 gtgtctttcg gaaaagcccc gtgtggccaa gttggcgtgc cagggtgtcta caccaacctc 720  
 tgcaaattca ctgagtggat agagaaaacc gtccaggcca gtttaa 765

&lt;210&gt; 525

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 525

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile  
 1 5 10 15  
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile  
 20 25 30  
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu

```

      35              40              45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
      50              55              60
Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
      65              70              75              80
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
      85              90              95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
      100             105             110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
      115             120             125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
      130             135             140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
      145             150             155             160
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
      165             170             175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
      180             185             190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
      195             200             205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
      210             215             220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
      225             230             235             240
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
      245             250

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<210> 526  
 <211> 963  
 <212> DNA  
 <213> Homo sapiens

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<400> 526
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aactgcatcg tgggtcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgacgc cattgacctg gccttatcca catccaccat gcctaagatc 240
cttgcccttt tctgggttga ttcccgagag attagctttg aggcctgtct taccagatg 300
ttctttattc atgccctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360
cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420
gcccagattg gcatcgaggc tgtgggtcgc ggatccctct tttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
caggatgtaa tgaagttggc ctatgcagac actttgcccc atgtggtata tggctcttact 600
gccattctgc tgggtcatggg cgtggacgta atgttcatct ccttgtccta ttttctgata 660
atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaaacctgt 720
gtgtcacaca ttggtgtggt actcgccttc tatgtgccac ttattggcct ctcaagttgta 780
caccgctttg gaaacagcct tcatcccatc gtgcgtgttg tcatgggtga catctacctg 840
ctgctgcctc ctgtcatcaa tcccatcatc tatggtgcc aaaccaaaca gatcagaaca 900
cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960
tga

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<210> 527  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 527

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
                                   5                                  10                                  15  
 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
                                   20                                  25                                  30  
 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
                                   35                                  40                                  45  
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
                                   50                                  55                                  60  
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
                                   65                                  70                                  75                                  80  
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
                                   85                                  90                                  95  
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
                                   100                                  105                                  110  
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
                                   115                                  120                                  125  
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
                                   130                                  135                                  140  
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu  
                                   145                                  150                                  155                                  160  
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
                                   165                                  170                                  175  
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu  
                                   180                                  185                                  190  
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
                                   195                                  200                                  205  
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val  
                                   210                                  215                                  220  
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
                                   225                                  230                                  235                                  240  
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
                                   245                                  250                                  255  
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg  
                                   260                                  265                                  270  
 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro  
                                   275                                  280                                  285  
 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala  
                                   290                                  295                                  300  
 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys

305  
<210> 528  
<211> 20  
<212> DNA  
<213> Homo Sapien  
  
<400> 528  
actatgggtcc agaggctgtg 20  
  
<210> 529  
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<213> Homo Sapien  
  
<400> 529  
atcacctatg tgccgcctct 20  
  
<210> 530  
<211> 1852  
<212> DNA  
<213> Homo sapiens  
  
<400> 530  
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tttctcttga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180  
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240  
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ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840  
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aacgtggctg cttggggaga ctacgatgac agcgccttca tggatcccag gtaccacgtc 960  
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gatctcatcg tcatgtctcag ggacacggat gtgaacaaga gggacaagca aaagaggact 1080  
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tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcactgatcc aaatattcca 1260  
gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa attaatggcc 1320  
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gcgaatttaa atgcgctgga tagatatgga agaactgctc tcataacttg tgtatgttgt 1500  
ggatcagcaa gtatagtcag ccctctactt gagcaaaatg ttgatgtatc ttctcaagat 1560  
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tttctgacta caaagaaaaa cagatgttaa aaatctcttc tgaaaacagc aatccagaac 1680  
aagacttaaa gctgacatca gaggaagagt cacaaaggct taaaggaagt gaaaacagcc 1740  
agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800  
tgggattccc agaaaacctg actaacggtg ccgctgctgg caatggtgat ga 1852  
  
<210> 531  
<211> 879

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

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aacgtgggca cttctggaga ccacaacgac tctctgttga agacgcttgg gagcaagagg 120
tgcaagtggg gctgccactg cttcccctgc tgcaggggga gcggcaagag caacgtgggtc 180
gcttggggag actacgatga cagcgccttc atggatccca ggtaccacgt ccatggagaa 240
gatctggaca agctccacag agctgcctgg tggggtaaag tccccagaaa ggatctcatc 300
gtcatgctca gggacacgga tgtgaacaag agggacaagc aaaagaggac tgctctacat 360
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cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgccaggaa 480
gatgaatgtg cgtaaatgtt gctggaacat ggcactgac caaatattcc agatgagtat 540
ggaaatacca ctctacacta tgctgtctac aatgaagata aattaatggc caaagcactg 600
ctcttatacg gtgctgatat cgaatcaaaa aacaagcatg gcctcacacc actgctactt 660
ggatatacatg agcaaaaaca gcaagtgggtg aaatttttaa tcaagaaaaa agcgaattta 720
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agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
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&lt;210&gt; 532

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

```

Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
      5              10              15

Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
      20              25              30

Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
      35              40              45

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
      50              55              60

Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
      65              70              75              80

Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
      85              90              95

Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
      100             105             110

Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
      115             120             125

Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
      130             135             140

Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
      145             150             155             160

Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
      165             170             175

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Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu  
 180 185 190

Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu  
 195 200 205

Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu  
 210 215 220

Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu  
 225 230 235 240

Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys  
 245 250 255

Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp  
 260 265 270

Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu  
 275 280 285

Val Ile Ile Met  
 290

<210> 533  
 <211> 801  
 <212> DNA  
 <213> Homo sapiens

<400> 533  
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 cctgcagcga gtgaggttg tggctgtgcc cccagctcct ggcacaccct cgcagagggtg 600  
 actggttgct ctttgagccc tcttagcctt gccagcatg cacaagcctc agtgctacta 660  
 ctgtgtctaca aatggagcca tataggggaa acgagcagcc atctcaggag caaggtgtat 720  
 gctgcctttg ggggctccag tccttgctc aagggtctta tgtcactgtg ggcttcttgg 780  
 ttgccaagag gcagaccata g 801

<210> 534  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 534  
 Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu  
 5 10 15

Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala  
 20 25 30

Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val  
           35                                  40                                  45  
 Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His  
           50                                  55                                  60  
 Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp  
           65                                  70                                  75                                  80  
 Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln  
                                   85                                  90                                  95  
 Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn  
                                   100                                  105                                  110  
 Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu  
           115                                  120                                  125  
 Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys  
           130                                  135                                  140  
 Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala  
           145                                  150                                  155                                  160  
 Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr  
                                   165                                  170                                  175  
 Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser  
                                   180                                  185                                  190  
 Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu  
           195                                  200                                  205  
 Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys  
           210                                  215                                  220  
 Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr  
           225                                  230                                  235                                  240  
 Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu  
                                   245                                  250                                  255  
 Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro  
           260                                  265

&lt;210&gt; 535

&lt;211&gt; 6082

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 535

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&lt;210&gt; 536

&lt;211&gt; 6140

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (4535)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 536

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&lt;210&gt; 537

&lt;211&gt; 1228

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 537

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Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
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Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
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Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
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Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu

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Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser	115	120	125
Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys	130	135	140
Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln	145	150	155
Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg	165	170	175
Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly	180	185	190
Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val	195	200	205
Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala	210	215	220
Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly	225	230	235
Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys	245	250	255
Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg	260	265	270
Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met	275	280	285
Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys	290	295	300
Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn	305	310	315
Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe	325	330	335
Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe	340	345	350
Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe	355	360	365
Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg	370	375	380

Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg  
 385 390 395 400  
 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr  
 405 410 415  
 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser  
 420 425 430  
 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly  
 435 440 445  
 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro  
 450 455 460  
 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln  
 465 470 475 480  
 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly  
 485 490 495  
 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala  
 500 505 510  
 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile  
 515 520 525  
 Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn  
 530 535 540  
 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp  
 545 550 555 560  
 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu  
 565 570 575  
 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His  
 580 585 590  
 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp  
 595 600 605  
 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly  
 610 615 620  
 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln  
 625 630 635 640  
 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu  
 645 650 655  
 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly  
 660 665 670  
 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu  
 675 680 685



Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr  
 690 695 700  
 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu  
 705 710 715 720  
 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser  
 725 730 735  
 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly  
 740 745 750  
 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr  
 755 760 765  
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu  
 770 775 780  
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys  
 785 790 795 800  
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn  
 805 810 815  
 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu  
 820 825 830  
 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu  
 835 840 845  
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile  
 850 855 860  
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg  
 865 870 875 880  
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr  
 885 890 895  
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp  
 900 905 910  
 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp  
 915 920 925  
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr  
 930 935 940  
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val  
 945 950 955 960  
 Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala  
 965 970 975  
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met  
 980 985 990  
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile

995                                      1000                                      1005  
 Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro  
     1010                                      1015                                      1020  
 Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val  
     1025                                      1030                                      1035                                      1040  
 Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu  
                                     1045                                      1050                                      1055  
 Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly  
                                     1060                                      1065                                      1070  
 Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu  
                                     1075                                      1080                                      1085  
 Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu  
     1090                                      1095                                      1100  
 Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile  
     1105                                      1110                                      1115                                      1120  
 Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp  
                                     1125                                      1130                                      1135  
 Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu  
                                     1140                                      1145                                      1150  
 Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr  
                                     1155                                      1160                                      1165  
 Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu  
     1170                                      1175                                      1180  
 Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile  
     1185                                      1190                                      1195                                      1200  
 Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln  
                                     1205                                      1210                                      1215  
 Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys  
                                     1220                                      1225  
  
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 <213> Homo sapiens  
  
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 Leu Gln Gly Phe Trp Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala  
                                     20                                      25                                      30  
 Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser  
                                     35                                      40                                      45

Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val  
 50 55 60  
 Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr  
 65 70 75 80  
 Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr  
 85 90 95  
 Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr  
 100 105 110  
 Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys  
 115 120 125  
 His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly  
 130 135 140  
 Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn  
 145 150 155 160  
 Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro  
 165 170 175  
 Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile  
 180 185 190  
 Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln  
 195 200 205  
 Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr  
 210 215 220  
 Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile  
 225 230 235 240  
 Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile  
 245 250 255  
 Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys  
 260 265 270  
 Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile  
 275 280 285  
 Val Phe Val Thr Phe Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr  
 290 295 300  
 Ala Ser Arg Val Phe Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu  
 305 310 315 320  
 Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala  
 325 330 335  
 Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile  
 340 345 350

Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His  
 355 360 365  
 Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr  
 370 375 380  
 Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val  
 385 390 395 400  
 Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu  
 405 410 415  
 Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile  
 420 425 430  
 Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser  
 435 440 445  
 Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val  
 450 455 460  
 Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly  
 465 470 475 480  
 Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln  
 485 490 495  
 Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile  
 500 505 510  
 Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg  
 515 520 525  
 His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr  
 530 535 540  
 Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile  
 545 550 555 560  
 Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu  
 565 570 575  
 Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn  
 580 585 590  
 Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn  
 595 600 605  
 Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro  
 610 615 620  
 Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro  
 625 630 635 640  
 Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln  
 645 650 655  
 Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile

660					665					670					
Phe	Leu	Ile	Leu	Leu	Asn	Thr	Ala	Ala	Gln	Val	Ala	Tyr	Val	Leu	Gln
	675						680					685			
Asp	Trp	Trp	Leu	Ser	Tyr	Trp	Ala	Asn	Lys	Gln	Ser	Met	Leu	Asn	Val
	690					695					700				
Thr	Val	Asn	Gly	Gly	Gly	Asn	Val	Thr	Glu	Lys	Leu	Asp	Leu	Asn	Trp
	705					710					715				720
Tyr	Leu	Gly	Ile	Tyr	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly
				725					730					735	
Ile	Ala	Arg	Ser	Leu	Leu	Val	Phe	Tyr	Val	Leu	Val	Asn	Ser	Ser	Gln
			740					745					750		
Thr	Leu	His	Asn	Lys	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu
		755					760					765			
Phe	Phe	Asp	Arg	Asn	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys
	770					775					780				
Asp	Ile	Gly	His	Leu	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe
	785					790					795				800
Ile	Gln	Thr	Leu	Leu	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala
			805					810						815	
Val	Ile	Pro	Trp	Ile	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe
			820					825					830		
Ile	Phe	Leu	Arg	Arg	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg
		835					840					845			
Leu	Glu	Ser	Thr	Thr	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser
	850					855					860				
Leu	Gln	Gly	Leu	Trp	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys
	865					870					875				880
Gln	Glu	Leu	Phe	Asp	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe
			885					890						895	
Leu	Phe	Leu	Thr	Thr	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile
			900					905					910		
Cys	Ala	Met	Phe	Val	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala
		915					920					925			
Lys	Thr	Leu	Asp	Ala	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu
	930					935					940				
Thr	Leu	Met	Gly	Met	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val
	945					950					955				960
Glu	Asn	Met	Met	Ile	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu
				965				970						975	

Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp  
 980 985 990  
 Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser  
 995 1000 1005  
 Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser  
 1010 1015 1020  
 Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser  
 1025 1030 1035 1040  
 Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp  
 1045 1050 1055  
 Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys  
 1060 1065 1070  
 Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met  
 1075 1080 1085  
 Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp  
 1090 1095 1100  
 Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro  
 1105 1110 1115 1120  
 Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val  
 1125 1130 1135  
 Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn  
 1140 1145 1150  
 Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr  
 1155 1160 1165  
 Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr  
 1170 1175 1180  
 Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys  
 1185 1190 1195 1200  
 Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr  
 1205 1210 1215  
 Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln  
 1220 1225 1230  
 Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg  
 1235 1240 1245  
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&lt;211&gt; 10

&lt;212&gt; PRT

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<223> Made in a lab

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<211> 14

<212> PRT

<213> Homo sapiens

<400> 541

Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu  
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<210> 542

<211> 15

<212> PRT

<213> Homo sapiens

<400> 542

Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
5 10 15

<210> 543

<211> 12

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<213> Homo sapiens

<400> 543

Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val  
5 10

<210> 544

<211> 18

<212> PRT

<213> Homo sapiens

<400> 544

Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe

199

5

10

15

Met Thr

&lt;210&gt; 545

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 545

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
                                   5                                  10                                  15

Ser Val

&lt;210&gt; 546

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 546

Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly  
                                   5                                  10                                  15

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met  
                                   20                                  25

&lt;210&gt; 547

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 547

Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu  
                                   5                                  10                                  15

Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu  
                                   20                                  25                                  30

Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys  
                                   35                                  40                                  45

Cys Arg Met Pro Arg Thr Leu Arg Arg Leu  
                                   50                                  55

&lt;210&gt; 548

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 548

Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu



200

5

10

15

Glu Cys

&lt;210&gt; 549

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 549

Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg  
5 10 15

Gln Ala

&lt;210&gt; 550

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 550

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe  
5 10

&lt;210&gt; 551

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 551

Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
1 5 10

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